

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 00:09:54 ; Search time 10 Seconds
(without alignments)
104.265 Million cell updates/sec

Title: US-09-913-772a-2

Perfect score: 1823

Sequence: 1 MKAFVFLNAPKDNWTYAGG.....DRRVEIEVKYKEVVTQPAG 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubpa/US10_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpa/US08_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpa/US11_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	5.2	417	1	US-10-858-730-227
2	93.5	5.1	229	1	US-10-510-386-228
3	93	5.1	410	1	US-10-793-626-3258
4	93	5.1	477	1	US-10-793-626-3250
5	84	4.6	1992	7	US-11-013-759-3
6	84	4.6	1992	7	US-11-013-759-13
7	84	4.6	2047	7	US-11-013-759-4
8	84	4.6	2047	7	US-11-013-759-7
9	84	4.6	2053	7	US-11-013-759-9
10	83.5	4.6	585	1	US-10-510-386-20
11	83.5	4.6	594	1	US-10-510-386-38
12	83.5	4.6	721	7	US-11-060-920-5
13	81.5	4.5	543	1	US-10-495-664-3
14	81	4.4	348	1	US-10-793-626-2866
15	79	4.3	334	1	US-10-802-796-728
16	79	4.3	444	7	US-11-074-176-170
17	78	4.3	259	1	US-10-510-386-108
18	76.5	4.2	251	7	US-11-054-515-1833
19	75	4.1	249	7	US-11-054-515-1753
20	75	4.1	524	7	US-11-082-389-10
21	73	4.0	1213	7	US-11-074-176-256
22	72.5	4.0	643	1	US-10-510-386-8
23	72	3.9	227	1	US-10-858-730-86
24	72	3.9	835	1	US-10-501-039-4
25	71.5	3.9	80	1	US-10-821-234-949

ALIGNMENTS

RESULT 1

US-10-858-730-227
; Sequence 227, Application US/10858730
; Publication No. US2005025568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; FILE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 227
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-858-730-227

Query Match 5.2%; Score 94; DB 1; Length 417;
Best Local Similarity 22.7%; Pred. No. 0.18;
Matches 66; Conservative 34; Mismatches 115; Indels 76; Gaps 13;

QY	59	VNPYLGFEGYDWMGRMAYKGSVDNGAFKAGQVLTAKLGYPTDLDLIVYTRLCGMVWRA	118
DB	93	VOPHSGSQANFAVYATLLEPGDTVLGMNLAHGHLTH--GSPVNFSGKLYNI---VPYGI	147
QY	119	DSKG--NYASTGVSRSEHD-----TGVSVPFAGGVAVTRDIATRL--EYOMVNIGDAGT	171
DB	148	DATGHIDYADLEKQAKEHKPKMIIGFSAYSGVDWAKMREIADSIGYLFVDMHVAVL	207
QY	172	VGTRPDNGMLSLGVSYRFQEDAAAPVAVAPAPAPAPV--ATKHFTLKSDVLFNFKATLK	229
DB	208	V-----AAGVYPNPVPFAHVVTTHHTKTLAG-----	233

Best Local Similarity 20.4%; Pred. No. 0.22;

3

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QY 215 LKSDVL--FNFNFKATLKPEQQALDQLYT---QLS-----NMDPKDGSVAVLGYTR 261
Db 262 IRLRLGNSARDNLKLSNNQSFVIASDGGQKNAKKLKTLAPSEKKEIVIDLK 321
QY 262 IGSE-----AYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMSENPVTGNT 308
Db 322 KGEKISLVNDKTVILPISNKEKSNKGNTP---KVS-----KILEGMNDNVINGNK 373
QY 309 CD 310
Db 374 FD 375

RESULT 5

US-11-013-759-3
Sequence 3, Application US/11013759
Publication No. US20050249747A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1992
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-11-013-759-3

Query Match 4.6%; Score 84; DB 7; Length 1992;
Best Local Similarity 20.1%; Pred. No. 11;
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;
QY 18 AGKLGWSQVHDTGYGNGFQNNNGPTRNDQLGAGA---FGGYQVNPYLG-----FEM 67
Db 959 SGLKAGKSTLNDGGL-----SIKNPTGSEIQVGADGVKFAKVNNGVVGAGIDGTTRI 1012
QY 68 GYDWLGRMAYKGSVDNG-----AFKAQGVQLT-AKLGYPTITDDLDIYTRLCGMVWR-- 117
Db 1013 TRDEIGFTGTNGSLDKSKPHLSKDGINAGGKITTNIQSGEIAQNSHDAVT--GGKIYDLK 1070
QY 118 -----ADSKGNVASTGVSRSEHDTGVSVPFAGGVWAVTRDI 154
Db 1071 TELENKISSTAKTAQNSLHFEVSADGQNNFTVSNPYSSYDT-----SKTSDV 1118
QY 155 ATRLEYQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAAPVAPAPAPAEVATKHFT 214
Db 1119 IT-----FAGENG-ITTKVNGVVRVIGDQTKG-----LTPKLTGVNNN 1157
QY 215 LKSDVLNFKATLKPEQQALDQLYTQLSNMDPKDGSVAVLGYTRIGSEAYNQOLSEK 274
Db 1158 GRGIVIDSQN-----GQNTITGLSNTLANVTNDRKGSVRTTEQGNIIKDE-----DKT 1204
QY 275 RAQSVVDYLVAKGIPAGKISARGMSES-----NPVTGNTC-----DNVKARAA 317
Db 1205 RAASIVDVLSA-----GFNLQNGEAVDFVSTYDTVNFADGNATTAKVYDDTTSKTV 1258
QY 318 LIDCLAPDRRVEIEVK--GYKEVVTOPAG 344
Db 1259 VYDNNVDDTTIEVKDKKLGKVTTLTSTG 1287

RESULT 6

US-11-013-759-13

Sequence 13, Application US/11013759
Publication No. US20050249747A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1992
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-11-013-759-13

Query Match 4.6%; Score 84; DB 7; Length 1992;
Best Local Similarity 20.1%; Pred. No. 11;
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;
QY 18 AGKLGWSQVHDTGYGNGFQNNNGPTRNDQLGAGA---FGGYQVNPYLG-----FEM 67
Db 959 SGLKAGKSTLNDGGL-----SIKNPTGSEIQVGADGVKFAKVNNGVVGAGIDGTTRI 1012
QY 68 GYDWLGRMAYKGSVDNG-----AFKAQGVQLT-AKLGYPTITDDLDIYTRLCGMVWR-- 117
Db 1013 TRDEIGFTGTNGSLDKSKPHLSKDGINAGGKITTNIQSGEIAQNSHDAVT--GGKIYDLK 1070
QY 118 -----ADSKGNVASTGVSRSEHDTGVSVPFAGGVWAVTRDI 154
Db 1071 TELENKISSTAKTAQNSLHFEVSADGQNNFTVSNPYSSYDT-----SKTSDV 1118
QY 155 ATRLEYQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAAPVAPAPAPAEVATKHFT 214
Db 1119 IT-----FAGENG-ITTKVNGVVRVIGDQTKG-----LTPKLTGVNNN 1157
QY 215 LKSDVLNFKATLKPEQQALDQLYTQLSNMDPKDGSVAVLGYTRIGSEAYNQOLSEK 274
Db 1158 GRGIVIDSQN-----GQNTITGLSNTLANVTNDRKGSVRTTEQGNIIKDE-----DKT 1204
QY 275 RAQSVVDYLVAKGIPAGKISARGMSES-----NPVTGNTC-----DNVKARAA 317
Db 1205 RAASIVDVLSA-----GFNLQNGEAVDFVSTYDTVNFADGNATTAKVYDDTTSKTV 1258
QY 318 LIDCLAPDRRVEIEVK--GYKEVVTOPAG 344
Db 1259 VYDNNVDDTTIEVKDKKLGKVTTLTSTG 1287

RESULT 7

US-11-013-759-4
Sequence 4, Application US/11013759
Publication No. US20050249747A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 4
; LENGTH: 2047
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-4

Query Match      4.6%; Score 84; DB 7; Length 2047;
Best Local Similarity 20.1%; Pred. No. 11;
Matches 78; Conservative 47; Mismatches 142; Indels 122; Gaps 17;

QY 18 AGCGLGWSQVHDTGFGYNGFQNNNGPTRNDQLGAGA-----FGGYQVNPYL-----FEM 67
Db 1014 SGLKAGKSTLNDGGL-----SIKNPTGSEQIQVGADGVKFAKNNNGVVGAGIDGTTRI 1067

QY 68 GYDNLGRMAYKGSVDNG-----AFKAQGVQLT-AKLGYPITDDLDIVTRLGGMVWR-- 117
Db 1068 TRDEIGFTGTNGSLDKSKPHLSKDGINAGGKKTNIQSGEIAQNSHDAVT--GGKIYDLK 1125

QY 118 -----ADSKGNVASTGVSRSEHDTGVSVPFAGGVEMAVTRDI 154
Db 1126 TELENKISSTAKTAQNSLHEFSVADEQGNFTVSNPYSSYDT-----SKTSDV 1173

QY 155 ATRLEYQWNNIGDAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVPAPAPAPAPAEVATKFT 214
Db 1174 IT-----FAGENG-ITTKVKNKGVVRVIGDQTKG-----LTTPKLTVGNNN 1212

QY 215 LKSDVLFNFKATLKPEGQOALDQLYTQLSNMDPKDGSVAVLGYTRIGSEAYNOOLSEK 274
Db 1213 GKGIVIDSQN-----GQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDE-----DKT 1259

QY 275 RAQSVVDVYLVAKGIPAGKISARGMGES-----NPVTGNTC-----DNVKARAA 317
Db 1260 RAASIVDVLSA-----GFNLQNGEAVDFVSTYDTVNFADGNATTAKVYDDTSKTSKV 1313

QY 318 LIDCLAPDRRVEIEVK--GYKEVVTOPAG 344
Db 1314 VYDVNVDDTTIEVKDKLGKVTTLTSTG 1342

RESULT 8
US-11-013-759-7
; Sequence 7, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; PRIOR FILING DATE: 2004-12-16
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-9

Query Match      4.6%; Score 84; DB 7; Length 2053;
Best Local Similarity 20.4%; Pred. No. 11;
Matches 76; Conservative 43; Mismatches 133; Indels 120; Gaps 17;

QY 39 NNNG-----PTRNDQLGAGAFG---GYQVNPYL-----FEMGYDNLGRMAYKGSVDNG 84
Db 1034 NNGLSIKNTASNEQIQVGADGVKFAKNNNGVVGAGIDGTTRIITRDEIGFTGTNGSLDKS 1093

QY 85 -----AFKAQGVQLT-AKLGYPITDDLDIVTRLGGMVWR----- 117
Db 1094 KPHLSKDGINAGGKKTNIQSGEIAQNSHDAVT--GGKIYDLKTELENKISSTAKTAQNS 1151

QY 118 -----ADSKGNVASTGVSRSEHDTGVSVPFAGGVEMAVTRDIATRLLEYQWNNIGDAGT 171
Db 1152 LHEFSVADEQGNFTVSNPYSSYDT-----SKTSDVIT-----FAGENG- 1190

QY 172 VQTRPDNGMLSLGVSYRFGQEDAAPVVPAPAPAPAPAEVATKFTLKSVDLNFNFKATLKPE 231
Db 1191 ITTKVKNKGVVRVIGDQTKG-----LTTPKLTVGNNGKGINVSNQ----- 1231

QY 232 GQOALDQLYTQLSNMDPKDGSVAVLGYTRIGSEAYNOOLSEKRAQSVVDVYLVAKGIPAG 291
Db 1232 GQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDE-----DKTRAASIVDVLSA----- 1279

QY 292 KISARGMGES-----NPVTGNTC-----DNVKARAAALIDCLAPDRRVEIEVK- 333
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Db 1280 GFNLQNGEAVDFVSTYDTNMFANGNTTTAKVTYDDT⁵SKTSKVYDVNVDDTTTIEVKDKK 1339

Qy 334 - GYKEVVTQ³PAG 344

Db 1340 LGVKT³TLTSTG 1351

```

RESULT 10
US/10-510-386-20
; Sequence 20, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Ramussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US/10-510-386-20

```

Query Match		4.6%	Score 83.5;	DB 1;	Length 585;
Best Local Similarity		26.1%;	Pred. No. 2.4;		
Matches 52; Conservative		20; Mismatches 70; Indels 57; Gaps 11;			
Qy	98	GYPITDDLDIYTRLCGMWRADSKGNVTASTGVRSRSEHDTGVSPFAGGVAVNRDIAIR	157 : : : : : : : : :		
Db	382	GYPVLDDRGGRL-NLFSAADGYAF-----TKNVTVTMSAKGGFH---TAD----	426 : : : : : : : : :		
Qy	158	LEYQWVNIGDAGTV-----GTRPDNGMLSLGVSVRFQEADA--PV	197 : : : : : : :		
Db	427	---RWRNDISGTGLTKKGTALKLEGDNITYSGGTRIQQGLEGSSETAFGRGDVALNGG	483 : : : : : : :		
Qy	198	VAPAPAP-----APEVATKHFTLKSDVLFNPNKATLKPEGOAALDLQLYTQLSN	245 : : : : : : :		
Db	484	ILXEDAPGKLIIEGDYQSAKGIIELQLSGKKOOLKIKGARL-K-GTLRLN--FT--DN	537 : : : : : : :		
Qy	246	MDPKDGSAVVLYTDRTGS	264 : : : : : :		
Db	538	YVPADGSAIIT-FRKRHGS	555 : : : : : :		

```

RESULT 11
US-10-510-386-38
; Sequence 38, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolbe
; TITLE OF INVENTION: Improved Bacilli
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/5
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-38

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Query Match
4.6%; Score 83.5; DB 1; Length 594;

	Best Local Similarity	26.1†	Pred. No. 2.4;		Indels	Gaps	
	Matches	52; Conservative	20; Mismatches	70; Indels	57; Gaps	11;	
Qy	98	GYPTDDLDITYRLGGWVRADSKGNVYASTGVSRSEHDTGVSVPFAGGVEMAVTRIATR	157				
Db	387	GYPLVDREGWGRL-NLPSAADGVGAP-----TKNVTVTMDSAKGGFH---TAD----	431				
Qy	158	LEYOVNNINIGDAGTV-----GTRPDNGMLSGVSYRFGQSDAA--PV	197				
Db	432	---RWNRNDISGTGLTKKGTCALKLECDNTYSGGTRIDQGTLEGGSETAFERGDDVALNGG	498				
Qy	198	VAPAPAP-----APEVATKHFTLKSDVLNFNFNKATIKPEQQOALDOLYTOLS	245				
Db	489	ILKEDAPGKLIIIEDYKQSAGKTLEQLSCKDKOLKIKGARLK--GTLFLN--FT--DN	542				
Qy	246	MDPKDGSAVVLYGTYDRIGS	264				
Db	543	YVPADGSALIIT-FRKRGHS	560				

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RESULT 12
US-11-060-920-5
; Sequence 5, Application US/11060920
; Publication No. US20050244378A1
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Paul L
; APPLICANT: Liu, Xuyang
; TITLE OF INVENTION: Method for Treating Glaucoma
; FILE REFERENCE: 960296.00149
; CURRENT APPLICATION NUMBER: US/11/060,920
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US 60/545,723
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 721
; TYPE: PRt
; ORGANISM: Clostridium botulinum
US-11-060-920-5

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Query Match	4.6%	Score 83.5;	DB 7;	Length 721;
Best Local Similarity	20.9%;	Pred. No. 3.1;		
Matches	71;	Conservative 39;	Mismatches 117;	Indels 113; Gaps 17;

Qy	2	KAJFVLNAAPKDNWTYAGGKLGWSQYHDTGFGVQ-----NGF--QNNNGPTRNDQLGAG	52
Db	165	KSKFIPN-----NTLFSNAKLKANANRDTDRDGIPEWEINGYVNMOKAVAMDDKPAAN	219
Qy	53	AFGGYQVN-----PYLGFEMGYDWLGRMAYKGSVDN-----GAFKAQGVQ	92
Db	220	GKKYKYSNPKPCTANDPYTDFE-----KVSQIDPFSVMVARDPMISAYPIVGVO	270
Qy	93	---LTKAGLYPITDDLDIYTRLGGMWVRADSKG-NVASTGVSRSEHDTGVSPVFAAGVVEW	148
Db	271	MEBLVVVSKSETITGDSST-----KSMKSTSHSTNINTVGAEVSGSLQLAGGIFP	320
Qy	149	AVTRDIAIATRLLEYOWVANNIGDAGVTGTRPDNGM-LSLUGVS-----VRFGEEDAAPVVAPA	201
Db	321	VFSMSASANYSHWTQNTSTVDDTTGSESPQGLSINTGESAYINPNRIYNTGTAPVYNVT	380
Qy	202	PAPAPEVATKHFTLKSVDLVLFNFNKATLKPEGOQAL-----D	237
Db	381	PT-----TTVIDKQSVATIK--QGESLIGDVLNPGGTYPPIEGPPMALNTMD	426
Qy	238	QL-----YTQLSNMDDPKDGSANVLGYVTDTRIGSEA-YN	268
Db	427	QFSRLIPINYNOLKSID--NGCTVMLSTSQFTGNPAKYN	464

RESULT 13
US-10-495-664-3
; Sequence 3, Application US/10495664

Publication No. US20050244416A1
; GENERAL INFORMATION:
; APPLICANT: JUNG, GUNDRAM
; TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE
; FILE REFERENCE: 034258-0801
; CURRENT APPLICATION NUMBER: US/10/495,664
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/EP02/12545
; PRIOR FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: DE 101 56 482.1
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: protein construct
US-10-495-664-3

Query Match 4.5%; Score 81.5; DB 1; Length 543;
Best Local Similarity 20.8%; Pred. No. 3.2;
Matches 64; Conservative 42; Mismatches 121; Indels 81; Gaps 15;
QY 7 LNAAPKDNNT--WYAGGKLGHSQYHDTGFGYNG-----FQNNNGPT-----RNDQLGAGAF 54
DB 229 MNSLQADDTAVVYCARDKGYYSYDMYDYGQGTVTTVSSASTKGPSPVFLAPSSSGQV 288
QY 55 GGYQVNPYL-----GFE-----MGYDVLGRMAYKGSVD--N 83
DB 289 KLOQSGPELVKPGASVKISKASGYAFSRSWMWVVKRPGQGLEWIGRI-YPGDGTNTN 347
QY 84 GAFKAQGVOLTA-----KLGYPIITDLDIYTRLGG-----MWMRADSKGNYASTGVS 130
DB 348 GKFKGKAT-LTADKSSSTAYMQVSSLTSDSAVYFCARGNTVVVPVPTMDYWGQGTITVVS 406
QY 131 RSEHDTGVSVPFAGGVWEAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGHLSLGVSYR-- 188
DB 407 SGGGGGGGGGGGGSDIELTQSPAS-----LAVSLGQRATISCRASESVDSYNSFMHW 461
QY 189 FGQEDAAPVVPAPAPAPAPAVATKHTLKDSDLFNFNKA-----TLKPEGQQAQDQLY 240
DB 462 YQKPKQPQ-----PKLLIYLAS---NLESGVPARFSGSGSRDTFTLTIDPVEADDAATY 513
QY 241 TQLSNMDP 248
DB 514 CQONNEDP 521

RESULT 14
US-10-793-626-2866
; Sequence 2866, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2866
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2866

Query Match 4.4%; Score 81; DB 1; Length 348;
Best Local Similarity 20.9%; Pred. No. 2;
Matches 77; Conservative 41; Mismatches 90; Indels 160; Gaps 22;
QY 12 KONTWAGKLGWSQYHDTGFGYNGFQNNNGPTNRNDQLGAGAFGGYQVNPYLGFEFG 68
DB 75 KDNNGYKNYTLK-AQEGKTEFYKNNFSNTLG-----YNGNLLGPTTLKKGDKV 122
QY 69 -----YDWLGRMAYKGSVDNG-----AFKAQGVQITAKLGY----- 99
DB 123 KIKLINLNDENTTFHHWG-LEVNGKYDGGPQSVQIKPKGKTIKFEYNQDSATLWYHPHS 181
QY 100 PITDDLDIYTRLGGMWMRADSKGNYASTGVSRSSEHDTGSPVFAAGGVEMAVTRD--IA 155
DB 182 PNTAK-QVYNGUSGLYIETDSKKNYP-----SDYGNKNDLFI-----IIQDKTFVS 226
QY 156 TRLEYQWNNIGDAGTVG-TRPDNGHLSLGVSYRFQGEDAAPVVPAPAPAPAVEATKHFT 214
DB 227 KKLNYSKTKD--EDGTQGDVTLVNGIVN-----PKLTTKEEK 261
QY 215 LKSDVLFNFNKATLKPEGQAQDQLYQLSNMDPKDGSVAVLGYTRDRIGSEAYNQOLSEK 274
DB 262 IRLRLT-----NGSNARD-LNLKLSN-----NQSF--- 285
QY 275 RAQSVVDVLVAKGIPAGKI-SARGHGESNPVTGNTCDNVKARAALDCLAPDRRVEI--- 330
DB 286 -----EYIASDG---GQLKNAKLUKEIN-----LAPSRKEKVID 317
QY 331 --EVKGYK 336
DB 318 LSKMKGEK 325

RESULT 15
US-10-802-796-728
; Sequence 728, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 728
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Mycobacterium sp.
US-10-802-796-728

Query Match 4.3%; Score 79; DB 1; Length 334;
Best Local Similarity 26.0%; Pred. No. 2.8;
Matches 44; Conservative 11; Mismatches 56; Indels 58; Gaps 8;
QY 18 AGGKLGWSQYHDTGTY-GNGFQNNNGPTNRNDQLGAGAFGGYQVNPYLGFEFG-YDWLGRM 75
DB 187 AGGAGGF-----GFLGGDGGAGNAGLLSSGGGFGGFGTAGGVGGAGNAGLWFG 240
QY 76 A-----YKGSVDNAGFAQGVQLTAKLGYPIITDLDIYTRLGGMWMRADSKGNYASTGVS 130

Db	241	AGGIGGIGNANGGAGNGGT-----GGOLWGGGAG--VEGGAA	278
Qy	131	RSEHDTGVSFPVFAGGVEMAVTRDIATPLEYQWVNNIGDAGTVGTRPDNG	179
Db	279	LSVGD TG-----GAGGVG-----GSAGLIGTGNGG	304

Search completed: November 26, 2005, 00:21:22
Job time : 11 secs

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QY 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTQAP 344
Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTQAP 344

RESULT 2

US-10-467-421-90
; Sequence 90, Application US/10467421
; Publication No. US20040116665A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Berthet, Philippe
; APPLICANT: Neyt, Cecile Anne
; APPLICANT: Poolman, Jan
; APPLICANT: Thonnard, Joelle
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45259
; CURRENT APPLICATION NUMBER: US/10/467,421
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01361
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103171.5
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 346
; TYPE: PRT
; ORGANISM: E. coli
US-10-467-421-90

Query Match 82.9%; Score 1511; DB 4; Length 346;

Best Local Similarity 84.9%; Pred. No. 1.3e-131;
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDQAGAGAGGGYQVNPYLG 65
Db 18 VAQAAPKDNWTYTGAKLGWSQYHDTGFI-----NNGPHTHENQAGAGAGGGYQVNPY 72
QY 66 EMGYDWMGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADSKGNYA 125
Db 73 EMGYDWMGRMPYKGSVENGAYKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADTSN-- 130
QY 126 STGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
Db 131 ---VYGNKNDTGVSPVFAGGVEYAITPEIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 187
QY 186 SYRFGQEDAAPVAP 245
Db 188 SYRFGQGEAAPVAP 247
QY 246 MDPKGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 248 LDPKGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLVAKGIPADKISARGMGESNPVT 307
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTQAP 342
Db 308 GNTCDNVKARAALIDCLAPDRRVEIEVKGKIDVVTQAP 344

RESULT 3

US-10-467-421-97
; Sequence 97, Application US/10467421
; Publication No. US20040116665A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Berthet, Philippe
; APPLICANT: Neyt, Cecile Anne
; APPLICANT: Poolman, Jan
; APPLICANT: Thonnard, Joelle
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45259

; CURRENT APPLICATION NUMBER: US/10/467,421
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01361
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103171.5
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 346
; TYPE: PRT
; ORGANISM: E. coli
US-10-467-421-97

Query Match 82.9%; Score 1511; DB 4; Length 346;

Best Local Similarity 84.9%; Pred. No. 1.3e-131;
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDQAGAGAGGGYQVNPYLG 65
Db 18 VAQAAPKDNWTYTGAKLGWSQYHDTGFI-----NNGPHTHENQAGAGAGGGYQVNPY 72
QY 66 EMGYDWMGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADSKGNYA 125
Db 73 EMGYDWMGRMPYKGSVENGAYKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADTSN-- 130
QY 126 STGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
Db 131 ---VYGNKNDTGVSPVFAGGVEYAITPEIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 187
QY 186 SYRFGQEDAAPVAP 245
Db 188 SYRFGQGEAAPVAP 247
QY 246 MDPKGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 248 LDPKGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLVAKGIPADKISARGMGESNPVT 307
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGKEVVTQAP 342
Db 308 GNTCDNVKARAALIDCLAPDRRVEIEVKGKIDVVTQAP 344

RESULT 4

US-10-946-647-1413
; Sequence 1413, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1413
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-946-647-1413

Query Match 82.9%; Score 1511; DB 5; Length 346;

Best Local Similarity 84.9%; Pred. No. 1.3e-131;
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTYAGKLGWSQYHDTGFGYNGFQNNNGPTRNDQAGAGAGGGYQVNPYLG 65
Db 18 VAQAAPKDNWTYTGAKLGWSQYHDTGFI-----NNGPHTHENQAGAGAGGGYQVNPY 72

Best Local Similarity 82.8%; Pred. No. 1.8e-130;
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;
QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNNNGPTRNDOLGAGAFGGYQVNPYLG 65
DB 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVGF 72
QY 66 EMGYDMLGRMAYKGSVDNGAFKAGQVLTAKLGYPITDLDIYTRLGGMWRADSKGNYA 125
DB 73 EMGYDMLGRMPYKGDNTNGAYKAGQVLTAKLGYPITDLDIYTRLGGMWRADTSNVP 132
QY 126 STGVSSEHDTGVSVPFAGGVEAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGV 185
DB 133 G-CASTKDHDTGVSVPFAGGIEVAITPEIATRLLEYQWNNIGDANTIGTRPDNGLLSVGV 191
QY 186 SYRFGQEDAAPVAP 245
DB 192 SYRFGQEDAAPVAP 251
QY 246 MDPKGSAAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
DB 252 LDPKGSAAVVLGYTDRIGSDAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 311
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 342
DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 348

RESULT 8
US-10-946-647-1389
; Sequence 1389, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; PRIOR FILING DATE: 2004-09-20
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1389
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Salmonella enterica
US-10-946-647-1389

Query Match 82.0%; Score 1495; DB 5; Length 350;
Best Local Similarity 82.8%; Pred. No. 4.1e-130;
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;
QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNNNGPTRNDOLGAGAFGGYQVNPYLG 65
DB 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVGF 72
QY 66 EMGYDMLGRMAYKGSVDNGAFKAGQVLTAKLGYPITDLDIYTRLGGMWRADSKGNYA 125
DB 73 EMGYDMLGRMPYKGDNTNGAYKAGQVLTAKLGYPITDLDIYTRLGGMWRADTSNVP 132
QY 126 STGVSSEHDTGVSVPFAGGVEAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGV 185
DB 133 G-GPSTKDHDTGVSVPFAGGIEVAITPEIATRLLEYQWNNIGDANTIGTRPDNGLLSVGV 191
QY 186 SYRFGQEDAAPVAP 245
DB 192 SYRFGQEDAAPVAP 251
QY 246 MDPKGSAAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
DB 252 LDPKGSAAVVLGYTDRIGSDAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 311

QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 342
DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 348

RESULT 9
US-10-946-647-1395
; Sequence 1395, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; CURRENT FILING DATE: 2004-09-20
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1395
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Salmonella enterica
US-10-946-647-1395

Query Match 82.0%; Score 1495; DB 5; Length 350;
Best Local Similarity 82.8%; Pred. No. 4.1e-130;
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;
QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNNNGPTRNDOLGAGAFGGYQVNPYLG 65
DB 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVGF 72
QY 66 EMGYDMLGRMAYKGSVDNGAFKAGQVLTAKLGYPITDLDIYTRLGGMWRADSKGNYA 125
DB 73 EMGYDMLGRMPYKGDNTNGAYKAGQVLTAKLGYPITDLDIYTRLGGMWRADTSNVP 132
QY 126 STGVSSEHDTGVSVPFAGGVEAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGV 185
DB 133 G-GPSTKDHDTGVSVPFAGGIEVAITPEIATRLLEYQWNNIGDANTIGTRPDNGLLSVGV 191
QY 186 SYRFGQEDAAPVAP 245
DB 192 SYRFGQEDAAPVAP 251
QY 246 MDPKGSAAVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
DB 252 LDPKGSAAVVLGYTDRIGSDAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 311
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 342
DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTOP 348

RESULT 10
US-10-946-647-1404
; Sequence 1404, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; CURRENT FILING DATE: 2004-09-20
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1404
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Salmonella enterica
US-10-946-647-1404

Query Match 82.0%; Score 1495; DB 5; Length 350;
Best Local Similarity 82.8%; Pred. No. 4.1e-130;
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;

QY 6 VLNAAPKONTWYAGGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVG 72

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125
73 EMGYDWLGRMPYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKSNP 132

QY 126 STGVSRSEHDTGVSPPVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 185
Db 133 G-GPSTKDHDTGVSPPVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 191

QY 186 SYRFGOSDRAVPVAP 245
Db 192 SYRFGQOEAAVPVAP 251

QY 246 MDPKGSVVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 252 LDPKGSVVVLGYTDRIGSDAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 311

QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQP 342
Db 312 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQP 348

RESULT 11

US-10-416-708A-24
; Sequence 24, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Fromknecht, Katja
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
; FILE REFERENCE: 37779-0004
; CURRENT APPLICATION NUMBER: US/10/416,708A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 24
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-24

Query Match 41.4%; Score 754; DB 4; Length 190;
Best Local Similarity 79.9%; Pred. No. 1.3e-61;
Matches 139; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

QY 6 VLNAAPKONTWYAGGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLG 65
Db 20 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVG 74

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125
Db 75 EMGYDWLGRMPYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKSN-- 132

QY 126 STGVSRSEHDTGVSPPVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 179
Db 133 ---VGKNHDTGVSPPVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 183

RESULT 12

US-10-416-708A-27
; Sequence 27, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Fromknecht, Katja
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
; FILE REFERENCE: 37779-0004
; CURRENT APPLICATION NUMBER: US/10/416,708A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-27

Query Match 41.4%; Score 754; DB 4; Length 192;
Best Local Similarity 79.9%; Pred. No. 1.3e-61;
Matches 139; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

QY 6 VLNAAPKONTWYAGGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLG 65
Db 20 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVG 74

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125
Db 75 EMGYDWLGRMPYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKSN-- 132

QY 126 STGVSRSEHDTGVSPPVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 179
Db 133 ---VGKNHDTGVSPPVAGGVEWAVTRDIATRLLEYQWNNIGDAGTVGTRPDNG 183

RESULT 13

US-10-416-708A-10
; Sequence 10, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Fromknecht, Katja
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
; FILE REFERENCE: 37779-0004
; CURRENT APPLICATION NUMBER: US/10/416,708A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-10

Query Match 41.0%; Score 748; DB 4; Length 194;
Best Local Similarity 79.8%; Pred. No. 4.9e-61;
Matches 138; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

QY 6 VLNAAPKONTWYAGGKLGWSQYHDTGFGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLG 65
Db 20 VAQAAPKONTWYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVG 74

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125
Db 75 EMGYDWLGRMPYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKSN-- 132

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OM protein - protein search, using sw model

Run on: November 25, 2005, 23:50:22 ; Search time 188 Seconds
(without alignments)
803.970 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAFVINAAPKONTWYAGS.....DRVEIEVKGYKEVVTQPAG 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1823	100.0	344	3 AAB18994	Aab18994 A P40 pol
2	1823	100.0	344	3 AAB08317	Aab08317 An outer
3	1823	100.0	344	3 AAY93341	Aay93341 Amino aci
4	1823	100.0	344	3 AAB08825	Aab08825 A P40 pol
5	1823	100.0	344	3 AAB18804	Aab18804 A Klebsie
6	1823	100.0	344	3 AAB08341	Aab08341 An outer
7	1823	100.0	344	3 AAB08368	Aab08368 Amino aci
8	1823	100.0	344	4 AAB67770	Aab67770 Amino aci
9	1823	100.0	344	5 AAM48395	Aam48395 Klebsiell
10	1823	100.0	344	5 AAM47796	Aam47796 Klebsiell
11	1823	100.0	344	8 ADI00532	Adi00532 Klebsiell
12	1823	100.0	344	8 ADI56807	Adi56807 K. pneumo
13	1823	100.0	344	8 ADI38366	Adi38366 K. pneumo
14	1818	99.7	344	2 AAR93797	Aar93797 Protein L
15	1818	99.7	452	4 AAB67771	Aab67771 Amino aci
16	1813	99.5	344	2 AAY44077	Aay44077 K.pneumon
17	1813	99.5	344	4 AAG67743	Aag67743 Amino aci
18	1813	99.5	344	4 AAB84122	Aab84122 Amino aci
19	1782	97.8	385	7 ABO60934	Abo60934 Klebsiell
20	1781	97.7	335	2 AAR88257	Aar88257 K.pneumon
21	1781	97.7	335	2 AAR95644	Aar95644 Klebsiell
22	1781	97.7	335	2 AAR93796	Aar93796 Protein P
23	1289	70.7	369	6 ABM69278	Abm69278 Photorhab
24	1279	70.2	384	7 ADF07637	Adf07637 Bacterial

25	1026	56.3	188	2 AAR93798	Aar93798 Protein L
26	984	54.0	179	2 AAR95645	Aar95645 Klebsiell
27	689	37.8	344	5 AAM50724	Aam50724 Haemophil
28	688	37.7	344	5 AAM50721	Aam50721 Haemophil
29	687	37.7	137	5 ABB83156	Abb83156 Partial O
30	687	37.7	153	5 AAE17872	Aae17872 Sequence
31	685	37.6	344	5 AAM50718	Aam50718 Haemophil
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33	684	37.5	344	5 AAM50717	Aam50717 Haemophil
34	684	37.5	344	5 AAM50716	Aam50716 Haemophil
35	684	37.5	344	5 AAM50722	Aam50722 Haemophil
36	683	37.5	344	5 AAM50725	Aam50725 Haemophil
37	680.5	37.3	341	5 AAM50720	Aam50720 Haemophil
38	680.5	37.3	341	5 AAM50723	Aam50723 Haemophil
39	680.5	37.3	341	5 AAM50726	Aam50726 Haemophil
40	678	37.2	344	5 AAM50727	Aam50727 Haemophil
41	671	36.8	364	3 AAB44588	Aab44588 Virulence
42	671	36.8	364	5 ABP54540	Abp54540 Actinobac
43	667	36.6	364	3 AAY97899	Aay97899 Actinobac
44	667	36.6	364	3 AAY96097	Aay96097 Actinobac
45	655.5	36.0	359	2 AAR66294	Aar66294 Non-typab

ALIGNMENTS

RESULT 1

AAB18994

ID AAB18994 standard; protein; 344 AA.

XX AAB18994;

DT 08-FEB-2001 (first entry)

XX A P40 polypeptide of Klebsiella pneumoniae.

P40; membrane fraction; Gram-negative bacteria; anticancer;

immune response; mononuclear blood cell; tumour necrosis factor-alpha; interleukin-12; antitumour; cancer.

XX Klebsiella pneumoniae.

WO2000054790-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000WO-FR000623.

PR 15-MAR-1999; 99FR-00003154.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

PI Libon C, Corvaia N, Beck A, Bonnefoy J;

WPI; 2000-587477/55.

DR N-PSDB; AAR96568.

XX Use of membrane fractions from Gram-negative bacteria as immunostimulants for the treatment or prevention of cancer, increases effect of e.g. chemotherapeutic agents.

PS Claim 6; Page 27-28; 34pp; French.

XX The present sequence represents a P40 polypeptide of Klebsiella

pneumoniae. The protein is found in the membrane fraction, and is used in the method of the invention. The specification describes the use of a

membrane fraction from Gram-negative bacteria for the preparation of an immunostimulating composition that can induce an anticancer immune

response. The membrane fraction not only stimulates proliferation of human mononuclear blood cells (immunostimulation) but also induces

production of tumour necrosis factor-alpha and interleukin (IL)-12, which are known to have antitumour activity, so that it improves the effects of

other co-administered anticancer treatments (chemotherapy or radiation).

Best Local Similarity 100.0%; P-Seq. NO. 1.3E-137;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Result No.	Score	Query		Length	DB	ID	Description
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1	1782	97.8	385	2	US-09-489-039A-7451	Sequence 7451, Ap	
2	1781	97.7	335	2	US-08-836-500A-2	Sequence 2, Appli	
3	1781	97.7	335	2	US-09-679-750-2	Sequence 2, Appli	
4	1279	70.2	384	2	US-09-543-681A-7922	Sequence 7922, Ap	
5	984	54.0	179	2	US-08-836-500A-4	Sequence 4, Appli	
6	984	54.0	179	2	US-09-679-750-4	Sequence 4, Appli	
7	671	36.8	364	2	US-09-809-665A-151	Sequence 151, App	
8	667	36.6	364	2	US-09-418-980-8	Sequence 8, Appli	
9	667	36.6	364	2	US-09-506-078-45	Sequence 45, Appli	
10	662.5	36.3	359	1	US-08-457-9978-2	Sequence 2, Appli	
11	662.5	36.3	359	2	US-08-467-722A-2	Sequence 2, Appli	
12	662.5	36.3	359	2	US-09-451-184-2	Sequence 2, Appli	
13	646.5	35.5	369	2	US-09-809-665A-153	Sequence 153, App	
14	639.5	35.1	369	2	US-09-418-980-10	Sequence 10, Appli	
15	639.5	35.1	369	2	US-09-506-078-46	Sequence 46, Appli	
16	586.5	32.2	338	1	US-08-210-394-1	Sequence 1, Appli	
17	379	20.8	72	2	US-08-836-500A-6	Sequence 6, Appli	
18	379	20.8	72	2	US-09-679-750-6	Sequence 6, Appli	
19	281	15.4	53	2	US-08-836-500A-8	Sequence 8, Appli	
20	281	15.4	53	2	US-09-679-750-8	Sequence 8, Appli	
21	242.5	13.3	379	2	US-09-328-352-5219	Sequence 5219, Ap	
22	231.5	12.7	351	2	US-09-252-991A-30094	Sequence 30094, A	
23	224.5	12.3	349	2	US-09-573-630A-2	Sequence 2, Appli	
24	200	11.0	342	2	US-09-902-540-15847	Sequence 15847, A	
25	199	10.9	335	2	US-09-252-991A-19595	Sequence 19595, A	
26	193.5	10.6	256	2	US-09-328-352-5775	Sequence 5775, Ap	
27	184.5	10.1	566	2	US-09-489-039A-14179	Sequence 14179, A	


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; STREET: 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,500A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PI81514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-500A-4
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; Query Match 54.0%; Score 984; DB 2; L
; Best Local Similarity 100.0%; Pred. No. 5.4e-90;
; Matches 179; Conservative 0; Mismatches 0;
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; DB 1 APKDNTRYAGGKLGWSQVHDTGFYNGFGONNNGPTRNDQL
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; QY 70 DWLGRMAYKGSVDNGAFKAQGQVLTAKLGYPIITDLDIYT
; DB 61 DWLGRMAYKGSVDNGAFKAQGQVLTAKLGYPIITDLDIYT
;
; QY 130 SRSEHDTGVSVPFAGGVHVAVTRDIATRLFYQWVNNIGDA
; DB 121 SRSEHDTGVSVPFAGGVHVAVTRDIATRLFYQWVNNIGDA
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; RESULT 6
; US-09-679-750-4
; Sequence 4, Application US/09679750
; Patent No. 6780420
; GENERAL INFORMATION:
; APPLICANT: Binz, Hans
; Baussant, Thierry
; Haeuw, Jean-Francois
; Nguyen Ngoc, Thien
;
; TITLE OF INVENTION: Carrier Protein Having an
; Effect, Immunogenic Compl
; Their Preparation, Nucleo
;
; Patent No. 6780420
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Rockey, Milnamow & Katz, Ltd.
; STREET: 180 N. Stetson, 2 Prudential Plaz
; 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/679,750
; FILING DATE: 08-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,500
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; REFERENCE/DOCKET NUMBER: PIE1514P0180US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-679-750-4

Query Match          54.0%; Score 984; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 5.4e-90;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APKDNWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYNPYLGFEMGY 69
DB 1 APKDNWYAGKLGWSQYHDTGYGNGFQNNNGPTRNDQLGAGAFGQYNPYLGFEMGY 60
QY 70 DMLGRMAYKGSVONGAFKAGQVLTAKLGYPIITDDLDIYTRLGGMWRADSKGNYSTGV 129
DB 61 DMLGRMAYKGSVONGAFKAGQVLTAKLGYPIITDDLDIYTRLGGMWRADSKGNYSTGV 120
QY 130 SRSEHDTGSPVPAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVSYR 188
DB 121 SRSEHDTGSPVPAGGVEMAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGMLSLGVSYR 179

RESULT 7
US-09-809-665A-151
; Sequence 151, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-09-809-665A-151

Query Match          36.8%; Score 671; DB 2; Length 364;
Best Local Similarity 42.4%; Pred. No. 2.6e-58;
Matches 153; Conservative 54; Mismatches 122; Indels 32; Gaps 10;

QY 1 MKAIFVLNAAPKDNWYAGKLGWSQYHDTGYGNGFQNNNGPTR-----NDQLGAGAFGG 56
DB 11 LSAAVAQAAPQONTFYAGAKAGWASFHDGIEQLDSAKNTDRGTYGINRNSVTYGVFGG 70
QY 57 YQV--NPYLGF--EMGYDMLGRM-----AYKGSVDNGAFK--AQGVLTAKLGYPIITDLD 106
DB 71 YQILNQDKLGLAAELGYDFGVRGSEKPKNGKADKKTFRHAAHGATIALKPSYEVLPLDLD 130
QY 107 IYTRLG-GMWRADSKGNVASTGVSRSEHDTGSPVPAGGVEMAVTRDIATRLLEYQWNN 165
DB 131 VYGVGIALVNNYTKTFNAAQEKVKTRRFQS--SLILGAGVEYAILPELAARVEYQWLN 188
QY 166 IGDA-----GTGVTTRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAP 217
DB 189 AGKASYSTLNRMGATDYRSDISSVSAGLSYRFGQ-GAVPVAAPA-----VETKNFAFS 241
QY 218 DVLFFNFKATLKPEGQQAALDQLYTLQSLNMDPKDGSVAVLGYTDRIGSEAYNQOLSEKRAQ 277
DB 242 DVLFAFGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIKESNLKLSORRAE 301
QY 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVGKYE 337
DB 302 TVANYIVSKGAPAAVNTAVGYGEANPVTGATCDKVKGRKALLIACIAPDRRVEVQVQTK 361
QY 338 V 338
DB 362 V 362

RESULT 8
US-09-418-980-8
; Sequence 8, Application US/09418980
; Patent No. 6713071
; GENERAL INFORMATION:
; APPLICANT: Campos, Manuel
; APPLICANT: Baarich, Mary Jo
; APPLICANT: Rosey, Everett
; APPLICANT: Ankenbauer, Robert
; APPLICANT: Warren-Stewart, Lynn
; APPLICANT: Suiter, Brian
; APPLICANT: Keach, Robin
; TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
; FILE REFERENCE: PC9854A
; CURRENT APPLICATION NUMBER: US/09/418,980
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-09-418-980-8

Query Match          36.6%; Score 667; DB 2; Length 364;
Best Local Similarity 42.1%; Pred. No. 6.5e-58;
Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;

QY 1 MKAIFVLNAAPKDNWYAGKLGWSQYHDTGYGNGFQNNNGPTR-----NDQLGAGAFGG 56
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QY 57 YQV--NPYLGF--EMGYDMLGRM-----AYKGSVDNGAFK--AQGVLTAKLGYPIITDLD 106
DB 71 YQILNQDKLGLAAELGYDFGVRGSEKPKNGKADKKTFRHAAHGATIALKPSYEVLPLDLD 130
QY 107 IYTRLG-GMWRADSKGNVASTGVSRSEHDTGSPVPAGGVEMAVTRDIATRLLEYQWNN 165
DB 131 VYGVGIALVNNYTKTFNAAQEKVKTRRFQS--SLILGAGVEYAILPELAARVEYQWLN 188
QY 166 IGDA-----GTGVTTRPDNGMLSLGVSYRFGQEDAAPVAPAPAPAPAPAPAPAPAPAP 217
DB 189 AGKASYSTLNRMGATDYRSDISSVSAGLSYRFGQ-GAVPVAAPA-----VETKNFAFS 241
QY 218 DVLFFNFKATLKPEGQQAALDQLYTLQSLNMDPKDGSVAVLGYTDRIGSEAYNQOLSEKRAQ 277
DB 242 DVLFAFGKSNLKPAAATALDAMQTEINNAGLSNAAIQVNGYTDRIKESNLKLSORRAE 301
QY 278 SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVGKYE 337
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Db 302 TVANYIVSKGAPAAVTVAVGGEANPVGTGCDKVKGRKALIACLAPDRRVEVQVGTKE 361
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Db 362 V 362

RESULT 9

US-09-506-078-45
; Sequence 45, Application US/09506078
; Patent No. 6911206
; GENERAL INFORMATION:
; APPLICANT: Pfizer Products Inc
; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CARRIERS THAT CAN INDUCE A
; FILE REFERENCE: DUAL IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/09/506,078
; CURRENT FILING DATE: 2000-02-16
; EARLIER APPLICATION NUMBER: N/A
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-09-506-078-45

Query Match 36.6%; Score 667; DB 2; Length 364;
Best Local Similarity 42.1%; Pred. No. 6.5e-58;
Matches 152; Conservative 54; Mismatches 123; Indels 32; Gaps 10;
Qy 1 MKAIFVLNAPKDNWTYAGGKLGWSQVYHDTGFGYNGFQNNNGPTR----NDQLGAGAFGG 56
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Qy 57 YQV--NPYLGF--EMGYDWLGRM----AYKGSVDNGAFK--AOGVOLITAKLGYPIITDLDL 106
Db 71 YQILNQDKLGLAAELGYDYFGRVRSKPKNGKADKTFRHAAGHATIALKPSYEVLPDLD 130
Qy 107 IYTRLG-GMWVRADSKGNVASTGVSRSEHDTGVSVPFAGVGEVAVTRDIATRLLEYQWNN 165
Db 131 VYGVGVIALVNTYTKTFNAAQEKVKTRRFOS--SLILGAGVEYAILPELAARVEYQWLNN 188
Qy 166 IGDA-----CTVGTTRPDNGMLSLGVSVRFGQEDAAPVVAAPAPAPAEVATKHTLKS 217
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Db 302 TVANYIVSKGAPAAVTVAVGGEANPVGTGCDKVKGRKALIACLAPDRRVEVQVGTKE 361
Qy 338 V 338
Db 362 V 362

RESULT 10

US-08-457-997B-2
; Sequence 2, Application US/08457997B
; Patent No. 5766608
; GENERAL INFORMATION:
; APPLICANT: Kolattukudy, P. E.
; TITLE OF INVENTION: Otitis Media Vaccine
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter and Griswold
; STREET: Suite 1800 800 Superior Avenue

; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2688
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,997B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Golrick, Mary E.
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8458
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-457-997B-2

Query Match 36.3%; Score 662.5; DB 1; Length 359;
Best Local Similarity 43.3%; Pred. No. 1.8e-57;
Matches 155; Conservative 49; Mismatches 121; Indels 33; Gaps 9;
Qy 1 MKAIFVLNAPKDNWTYAGGKLGWSQVYHDTGFGYNGFQNNNGPTRNDQLGAGAFGG 56
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Qy 57 YQV--NPYLGFEMGYDWLGRMAYKGSVDNGAFKAO----GVQLTAKLGYPIITDLDIY 108
Db 73 YQILNQDNFGLAAELGYDDFGRAKLR---EAGPKAKHTNHGAYLSLKGSYEVLGDLVY 129
Qy 109 IRLGGMWRADSKGNVASTGV---SRSEHDTGVSVPFAGVGEVAVTRDIATRLLEYQWNN 165
Db 130 GRAGVALVRSYDKFYEDANGTRDHKKGRHTARASGLFAVGAEYAVLPELAVRLEYQWLTR 189
Qy 166 IG-----DAGTVGTTRPDNGMLSLGVSVRFGQEDAAPVVAAPAPAPAEVATKHTLKS 218
Db 190 VYKRPQDKPNTAINYNPWIGCINAGISYRFGQGE-APVVA-----APENVSKTFLNSD 243
Qy 219 VLFNFKNATLKPEGOQALDQLYTQLSNMDDPKDGSVVLGYTDRIIGSEAYNQOLSKRAQS 278
Db 244 VTFAGKANLKPQAQATLDSVYGEISQV--KSRKVAVAGYTNRIGSDAFNVKLSQERADS 301
Qy 279 VVDYLVAKGIIPAGKISARGNGSNPVGTGNTCDNVKARAALIDCLAPDRRVEIEVKGYK 336
Db 302 VANYFVAKGAAADAISATGYGEANPVGTGCDQVKGRKALIACLAPDRRVEIANGTK 359

RESULT 11

US-08-467-722A-2
; Sequence 2, Application US/08467722A
; Patent No. 6030626
; GENERAL INFORMATION:
; APPLICANT: Kolattukudy, P. E.
; TITLE OF INVENTION: Otitis Media Vaccine
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter and Griswold
; STREET: Suite 1800 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2688
; COMPUTER READABLE FORM:

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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uspto)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2005, 23:51:17 ; Search time 230 Seconds
(without alignments)
1055.225 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAIFVLNAPKDNWTYAGG.....DRRVIEVKGKVVTPAQ 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1813	99.5	344	1 OMPA_KLEPN	P24017 klebsiella
2	1542	84.6	350	1 OMPA_ENTAE	P09146 enterobacte
3	1525.5	83.7	351	1 OMPA_SHIDY	P02935 shigella dy
4	1513.5	83.0	347	2 Q52JK5_ENTSA	Q52JK5 enterobacte
5	1511	82.9	346	1 OMPA_ECO57	P0a910 escherichia
6	1511	82.9	346	1 OMPA_ECOLI	P0a910 escherichia
7	1511	82.9	346	2 Q6W821_SHISO	Q6w821 shigella so
8	1507	82.7	346	2 Q6PNM6_SHIBO	Q6pnm6 shigella bo
9	1505	82.6	346	2 Q9L6J0_ECOLI	Q9lj0 escherichia
10	1501	82.3	350	2 Q57OT3_SALCH	Q57qt3 salmonella
11	1500	82.3	350	2 Q5PGD5_SALPA	Q5pgd5 salmonella
12	1499	82.2	350	1 OMPA_SALTI	Q8z780 salmonella
13	1495	82.0	350	1 OMPA_SALTY	P02936 salmonella
14	1487	81.6	379	2 Q8CW76_ECOL6	Q8cw76 escherichia
15	1473	80.8	348	2 Q83RX2_SHIFL	Q83rx2 shigella fl
16	1466	80.4	327	2 Q7X017_SHIFL	Q7x017 shigella fl
17	1381.5	75.8	359	1 OMPA_SERMA	P04845 serratia ma
18	1364	74.8	319	2 Q6QT47_SALGL	Q6qt47 salmonella
19	1325.5	72.7	353	1 OMPA_YERPE	Q8z777 versinia pe
20	1325.5	72.7	353	1 OMPA_YERPS	P38399 versinia ps
21	1306	71.6	366	2 Q6D6D4_ERMCT	Q6d6d4 erwinia car
22	1289	70.7	368	2 Q7N602_PHOLL	Q7n602 photorhabdu
23	1262.5	69.3	367	2 Q9RM69_ERWCA	Q9rm69 erwinia car
24	1128.5	61.9	238	1 Q9N114_ESCVU	Q9n114 escherichia
25	1112.5	61.0	244	2 Q47880_ESCVU	Q47880 escherichia
26	1111	60.9	243	1 OMPA_ESCFE	P24747 escherichia
27	1110.5	60.9	244	2 Q9N115_ESCVU	Q9n115 escherichia
28	1106	60.7	243	1 OMPA_ESCHE	P24754 escherichia
29	1095.5	60.1	238	2 Q9N123_ENTAE	Q9n123 enterobacte
30	1089	59.7	241	1 OMPA_ESCBL	Q9N124 escherichia
31	1056.5	58.0	238	1 OMPA_CITFR	P24016 citrobacter

RESULT 1

ID	OMPA_KLEPN	STANDARD	PRT	344 AA.
AC	P24017	O69435		
DT	01-MAR-1992	(Rel. 21, Created)		
DT	15-DEC-1998	(Rel. 37, Last sequence update)		
DT	13-SEP-2005	(Rel. 48, Last annotation update)		
DE	Outer membrane protein A precursor (Outer membrane protein II).			
GN	Name=ompA;			
OS	Klebsiella pneumoniae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Klebsiella.			
OX	NCBI_TaxID=573;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=RV 308;			
RX	MEDLINE=98192544; PubMed=9524233; DOI=10.1016/S0378-1119(98)00060-2;			
RA	Nguyen T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A.,			
RA	Bausant T., Haeuw J.P., Uhlen M., Binz H., Stahl S.;			
RT	"Chromosomal sequencing using a PCR-based biotin-capture method			
RT	allowed isolation of the complete gene for the outer membrane protein			
RT	A of Klebsiella pneumoniae.";			
RL	Gene 210:93-101(1998).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE OF 93-335.			
RC	STRAIN=LD119;			
RX	MEDLINE=92065252; PubMed=1955870;			
RA	Lawrence J.G., Ochman H., Hartl D.L.;			
RT	"Molecular and evolutionary relationships among enteric bacteria.";			
RL	J. Gen. Microbiol. 137:1911-1921(1991).			
CC	- FUNCTION: Required for the action of colicins K and L and for the			
CC	stabilization of mating aggregates in conjugation. Serves as a			
CC	receptor for a number of I-even like phages. Also acts as a porin			
CC	with low permeability that allows slow penetration of small			
CC	solutes (by similarity).			
CC	- SUBUNIT: Monomer (Probable).			
CC	- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.			
CC	- SIMILARITY: Belongs to the ompA family.			
CC	- SIMILARITY: Contains 1 OmpA-like domain.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	EMBL; AJ000998; CAA04450.1; -; Genomic DNA.			
DR	EMBL; M63355; AAA25119.1; -; Genomic DNA.			
DR	HSSP; P02934; 1QJP.			
DR	SMR; P24017; 10-195.			
DR	InterPro; IPR006664; Bac_OmpA.			
DR	InterPro; IPR002368; OmpA.			
DR	InterPro; IPR006665; OmpA/MotB.			
DR	InterPro; IPR006690; OMPA_LIKE.			

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DR InterPro; IPR000498; OmpA_tmem.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA_membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMEMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA_1; 1.
DR PROSITE; PS11123; OmpA_2; 1.
KW Conjugation; Ion transport; Membrane; Outer membrane;
KW Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.
FT SIGNAL 1 ?
FT CHAIN ? 344
FT TRANSMEM 15 28
FT TRANSMEM 48 60
FT TRANSMEM 63 78
FT TRANSMEM 90 100
FT TRANSMEM 104 119
FT TRANSMEM 140 151
FT TRANSMEM 157 173
FT TRANSMEM 179 190
FT REPEAT 199 200
FT REPEAT 201 202
FT REPEAT 203 204
FT REPEAT 205 206
FT DOMAIN 208 336
FT REGION 199 206
FT DISULFID 309 321
FT CONFLICT 335 335
SQ SEQUENCE 344 AA; 37061 MW; AC88AAE3B7871B16 CRC64;

Query Match 99.5%; Score 1813; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-131; Indels 0; Gaps 0;
Matches 342; Conservative 0; Mismatches 0;

Qy 1 MKAIFVLNAAPKONTWYAGKLGWSQVHDTGFGYNGFQNNNGPTRNDQLGAGAFGGYQYN 60
Db 1 MKAIFVLNAAPKONTWYAGKLGWSQVHDTGFGYNGFQNNNGPTRNDQLGAGAFGGYQYN 60
Qy 61 PYLGFENGWDLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDLDIYTRLGGWVRADS 120
Db 61 PYLGFENGWDLGRMAYKGSVDNGAFKAQGVLTAKLGYPTDLDIYTRLGGWVRADS 120
Qy 121 KGNVASTGVSRSHTDGVSPVFAAGVWEAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGM 180
Db 121 KGNVASTGVSRSHTDGVSPVFAAGVWEAVTRDIATRLLEYQWNNIGDAGTVGTRPDNGM 180
Qy 181 LSLGVSYRFQGEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240
Db 181 LSLGVSYRFQGEDAAPVAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 240
Qy 241 TQLSNMDPKDGSVAVLYGTDRISEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
Db 241 TQLSNMDPKDGSVAVLYGTDRISEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGE 300
Qy 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEVEVGYKEVVTQP 342
Db 301 SNPVTGNTCDNVKARAALIDCLAPDRRVEVEVGYKEVVTQP 342

RESULT 2
OMPA_ENTAE STANDARD; PRT; 350 AA.
AC P09146;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Outer membrane protein A precursor.
GN Name=ompA;
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
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KW	Conjugation; Ion transport; Membrane; Outer membrane; Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.	1	21	
FT	SIGNAL	22	351	Outer membrane protein A.
FT	CHAIN	27	40	Potential.
FT	TRANSMEM	55	67	Potential.

QY 6 VLNAAPKDNWYAGGKLGWSQYHDTGFYGNQFQNNNGPTRNDQLGAGAFGGYQVNPYLG 65

Db 248 LDPKDSVVLGYDTRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMESNPVT 307
Qy 306 GNTCDNVKQRAALIDCLAPRRVEIEVKGKVVVTP 342
Db 308 GNTCDNVKQRAALIDCLAPRRVEIEVKGKIDVVTP 344

RESULT 6
OMP_A_ECOLI
ID OMP_A_ECOLI STANDARD; PRT; 346 AA.
AC POA9IO; P02934;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Outer membrane protein A precursor (Outer membrane protein II*)
OS Names: ompA; Synonyms: con, tolG, cut; OrderedLocNames: b0957;
OC Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K12;
RX MEDLINE=81053729; PubMed=6253901;
RA Beck E., Bremer E.;
RT "Nucleotide sequence of the gene ompA coding the outer membrane protein II of Escherichia coli K-12";
RL Nucleic Acids Res. 8:3011-3024 (1980).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K12;
RX MEDLINE=81170587; PubMed=6260961;
RA Movva N.R., Nakamura K., Inouye M.;
RT "Gene structure of the OmpA protein, a major surface protein of Escherichia coli required for cell-cell interaction";
RL J. Mol. Biol. 143:317-328 (1980).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Ohnina T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map";
RL DNA Res. 3:137-155 (1996).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MGL655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474 (1997).
RN [5]
RP PROTEIN SEQUENCE OF 22-346.
RC STRAIN=K12;
RX MEDLINE=81054820; PubMed=7001461;
RA Chen R., Schmidmayr W., Kramer C., Chen-Schmeisser U., Henning U.;
RT "Primary structure of major outer membrane protein II (ompA protein) of Escherichia coli K-12";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4592-4596 (1980).
RN [6]
RP PROTEIN SEQUENCE OF 22-34.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;

RT "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12";
RL Electrophoresis 18:1259-1313 (1997).
RN [7]
RP PROTEIN SEQUENCE OF 22-32.
RC STRAIN=K12 / W3110;
RA Pasquali C., Sanchez J.-C., Ravier F., Golaz O., Hughes G.J., Frutiger S., Paquet N., Wilkins M., Appel R.D., Bairoch A., Hochstrasser D.F.;
RL Submitted (SEP-1994) to Swiss-Prot.
RN [8]
RP PROTEIN SEQUENCE OF 22-26.
RC STRAIN=K12 / W3110;
RX MEDLINE=98291876; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M., Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RT "Extraction of membrane proteins by differential solubilization for separation using two-dimensional gel electrophoresis";
RL Electrophoresis 19:837-844 (1998).
RN [9]
RP MUTANTS RESISTANT TO PHAGE ENTRY.
RX MEDLINE=84264337; PubMed=6086577;
RA Morona R., Klose M., Henning U.;
RT "Escherichia coli K-12 outer membrane protein (OmpA) as a bacteriophage receptor: analysis of mutant genes expressing altered proteins";
RL J. Bacteriol. 159:570-578 (1984).
RN [10]
RP MUTANTS RESISTANT TO PHAGE ENTRY.
RX MEDLINE=86033606; PubMed=3902787;
RA Morona R., Kramer C., Henning U.;
RT "Bacteriophage receptor area of outer membrane protein OmpA of Escherichia coli K-12";
RL J. Bacteriol. 164:539-543 (1985).
RN [11]
RP PORIN ACTIVITY.
RC STRAIN=K12;
RX MEDLINE=92129334; PubMed=1370823;
RA Sugawara E., Nikaido H.;
RT "Pore-forming activity of OmpA protein of Escherichia coli";
RL J. Biol. Chem. 267:2507-2511 (1992).
RN [12]
RP SUBCELLULAR LOCATION.
RX PubMed=7813480;
RA Kuhn A., Kiefer D., Koehne C., Zhu H.-Y., Tschantz W.R., Dalbey R.E.;
RT "Evidence for a loop-like insertion mechanism of pro-Omp A into the inner membrane of Escherichia coli";
RL Eur. J. Biochem. 226:891-897 (1994).
RN [13]
RP TOPOLOGY.
RX MEDLINE=94148615; PubMed=8106193;
RA Gromiha M.M., Ponnusamy P.K.;
RT "Prediction of transmembrane beta-strands from hydrophobic characteristics of proteins";
RL Int. J. Pept. Protein Res. 42:420-431 (1993).
RN [14]
RP TOPOLOGY.
RX MEDLINE=99296577; PubMed=10368142;
RA Koebnik R.;
RT "Structural and functional roles of the surface-exposed loops of the beta-barrel membrane protein OmpA from Escherichia coli";
RL J. Bacteriol. 181:3688-3694 (1999).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 22-192.
RX MEDLINE=99023200; PubMed=9808047;
RA Fautsch A., Schulz G.E.;
RT "Structure of the outer membrane protein A transmembrane domain";
RL Nat. Struct. Biol. 5:1013-1017 (1998).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=20229895; PubMed=10764596; DOI=10.1006/jmbi.2000.3671;
RA Fautsch A., Schulz G.E.;
RT "High-resolution structure of the OmpA membrane domain";

RL J. Mol. Biol. 298:273-282 (2000).
 RN [17]
 RP STRUCTURE BY NMR OF 22-197.
 RX PubMed=11276254; DOI=10.1038/86214;
 RA Arora A., Abildgaard F., Bushweller J.H., Tamm L.K.;
 RT "Structure of outer membrane protein A transmembrane domain by NMR
 RT spectroscopy.";
 RN Nat. Struct. Biol. 8:334-338 (2001).
 RN [18]
 RP MASS SPECTROMETRY.
 RX MEDLINE=20222957; PubMed=10757971; DOI=10.1021/b1000150m;
 RA le Coutre J., Whiteledge J.P., Gross A., Turk E., Wright E.M.,
 RA Kaback H.R., Faull K.F.;
 RT "Proteomics on full-length membrane proteins using mass
 RT spectrometry.";
 RL Biochemistry 39:4237-4242 (2000).
 CC -/- FUNCTION: Required for the action of colicins K and L and for the
 CC stabilization of mating aggregates in conjugation. Serves as a
 CC receptor for a number of T-even like phages. Also acts as a porin
 CC with low permeability that allows slow penetration of small
 CC solutes.
 CC -/- SUBUNIT: Monomer (Probable).
 CC -/- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -/- MASS SPECTROMETRY: MW=35177; METHOD=Electrospray; RANGE=22-346;
 CC NOTE=Ref.18.
 CC -/- SIMILARITY: Belongs to the ompA family.
 CC -/- SIMILARITY: Contains 1 OmpA-like domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC removed.
 CC -----
 DR EMBL; V00307; CAA23588.1; -; Genomic DNA.
 DR EMBL; D90733; BAA35715.1; -; Genomic DNA.
 DR EMBL; D90734; BAA35722.1; -; Genomic DNA.
 DR EMBL; U00096; AAC74043.1; -; Genomic_DNA.
 DR F1R; A93707; MRECA.
 DR PDB; 1BXW; X-ray; A=22-192.
 DR PDB; 1G90; NMR; A=22-197.
 DR PDB; 1QJP; X-ray; A=22-192.
 DR SWISS-2DPAGE; POA910; COLI.
 DR ECO2DBASE; F024.5; 6TH EDITION.
 DR ECO2DBASE; F028.0; 6TH EDITION.
 DR ECO2DBASE; F033.0; 6TH EDITION.
 DR ECO2DBASE; F033.1; 6TH EDITION.
 DR EcoGene; EH0663; -.
 DR EcoGene; EH0669; ompA.
 DR InterPro; IPR006664; Bac OmpA.
 DR InterPro; IPR002368; OmpA.
 DR InterPro; IPR006665; OmpA/MotB.
 DR InterPro; IPR006690; OMPA LIKE.
 DR InterPro; IPR000498; OmpA_tmemb.
 DR Pfam; PF00691; OmpA; 1.
 DR Pfam; PF01389; OmpA membrane; 1.
 DR PRINTS; PR01021; OMPADOMAIN.
 DR PRINTS; PR01022; OUTRMBRANE.
 DR ProDom; PD000930; OmpA/MotB; 1.
 DR PROSITE; PS01068; OMPA_1; 1.
 DR PROSITE; PS1123; OMPA_2; 1.
 KW 3D-structure; Complete proteome; Conjugation;
 KW Direct protein sequencing; Ion transport; Membrane; Outer membrane;
 KW Phage recognition; Porin; Repeat; Signal; Transmembrane; Transport.

Query Match 82.9%; Score 1511; DB 1; Length 346;
 Best Local Similarity 84.9%; Pred. No. 1-2e-107;
 Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;
 QY 6 VLNAAPKNDNTWYAGKLGWSQYHDTGFGYNGFNQNNPTNRNDQLGAGAFGGYQVNPYLGF 65
 Db 18 VAQAAPKNDNTWYTGAKLGWSQYHDTGFI-----NNGPHTHENQLGAGAFGGYQVNPYVGF 72

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTITDDLDIYTRLGGMVWRADSKGNYA 125
 Db 73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPTITDDLDIYTRLGGMVWRADTKSN -- 130
 QY 126 STGVSRSEHDTGVSFVAGGVWAVTRDIATRLVQVWNNIGDAGTVGTRPDNGMLSLGV 185
 Db 131 --VYGNKNDTGVSPFVAGGVVATPEIATRLVQVWNNIGDAGTVGTRPDNGMLSLGV 187
 QY 186 SYRFGQEDAAVVPAPAPAPAPAPVATKHTLKSDVLFNFNKTLPKPGQQAALDOLYTOLSN 245
 Db 188 SYRFGQGEAAVVPAPAPAPAPVQTKHTLKSDVLFNFNKTLPKPGQAALDOLYSOLSN 247
 QY 246 MPKKGSAVVLGYTDRIIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGMGESNPVT 305
 Db 248 LDPKGSVVVLGYTDRIIGSDAYNQGLSERRAQSVVDYLVAKGIPADKISARGMGESNPVT 307
 QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTPQ 342
 Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKIKDVVTPQ 344
 RESULT 7
 Q6W821 SHISO
 ID Q6W821 SHISO PRELIMINARY; PRT; 346 AA.
 AC Q6W821;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Outer membrane protein A precursor.
 GN Name=ompA;
 OS Shigella sonnei.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OC NCBI_TaxID=624;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=USMSS2;
 RA Kirpal-Kaur B., Mohd Zaki S., Asma I., Ravichandran M.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY05874; AAP74759.1; -; Genomic_DNA.
 DR SMR; Q6W821; 22-197.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR006664; Bac OmpA.
 DR InterPro; IPR001035; MotF.
 DR InterPro; IPR002368; OmpA.
 DR InterPro; IPR006665; OmpA/MotB.
 DR InterPro; IPR006690; OMPA LIKE.
 DR Pfam; PF00691; OmpA; 1.
 DR Pfam; PF01389; OmpA membrane; 1.
 DR PRINTS; PR01023; NAFLGMOTY.
 DR PRINTS; PR01021; OMPADOMAIN.
 DR PRINTS; PR01022; OUTRMBRANE.
 DR ProDom; PD000930; OmpA/MotB; 1.
 DR PROSITE; PS01068; OMPA; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 346 AA; 37201 MW; 195147734CDF8B04 CRC64;
 Query Match 82.9%; Score 1511; DB 2; Length 346;
 Best Local Similarity 84.9%; Pred. No. 1-2e-107;
 Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;
 QY 6 VLNAAPKNDNTWYAGKLGWSQYHDTGFGYNGFNQNNPTNRNDQLGAGAFGGYQVNPYLGF 65
 Db 18 VAQAAPKNDNTWYTGAKLGWSQYHDTGFI-----NNGPHTHENQLGAGAFGGYQVNPYVGF 72
 QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTITDDLDIYTRLGGMVWRADSKGNYA 125
 Db 73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPTITDDLDIYTRLGGMVWRADTKSN -- 130

D	b		131	---	-VGKKNHDTGVSVPFAGGVVEYAITPEIATRLERYQWVNNIGDAHTIGTRPDNGMLSLGV	18
Q	y		186	SYRFGQEDAAAPVAPAPAPAEVATKHFTLKSDVLNFENKATLKPEGQAALDQLYTQLSN	245	
D	b		188	SYRFGQGEAAPVAPAPAPAEVQTKHFTLKSDVLNFENKATLKPEGQAALDQLYSOLSN	247	
Q	y		246	MDPKDGSAVLGYGTDRIQSEAYNQOLSSEKRASQSVVDYLVAKGIPAGKISAROMGSNPVT	305	
D	b		248	LDPKDGSSVVLGYTDRIGSDAYNOGLSRRASQSVVDYLISKGIPDKISARGMGSPNPT	307	
Q	y		306	GNTCDNVKARAALIDCLAPDRRVIEVKGYKEVVTPQ	342	
D	b		308	GNTCDNVKQRAALIDCLAPDRRVIEVKGIKDQVVTQP	344	
 RESULT 9						
Q	9	L6J0	Ecoli			
I	D	Q9L6J0	Ecoli	PRELIMINARY;	PRT; 346 AA.	
A	C	Q9L6J0;				
D	T	01-OCT-2000	(TrEMBLrel. 15, Created)			
D	T	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)			
D	T	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
D	E		Outer membrane protein A.			
G	N	Name=ompA;				
O	S	Escherichia coli.				
O	C	Bacteria; Proteobacteria;	Gammaaproteobacteria; Enterobacteriales;			
O	C	Enterobacteriaceae;	Escherichia.			
O	X	NCBI_TaxID=562;				
R	N	[1]				
R	P	NUCLEOTIDE SEQUENCE.				
R	C	STRAIN=RS218;				
R	A	Wang Y., Kim K.S.;				
R	L	Submitted (FEB-2000)	to the EMBL/GenBank/DBJ databases.			
D	R	EMBL; AF234269;	AAF37887.1; -; Genomic_DNA.			
D	R	HSSP; P02934;	1QJP.			
D	R	SMR; Q9L6J0;	22-197.			
D	R	GO; GO:0016021;	C:integral to membrane; IEA.			
D	R	GO; GO:0009279;	C:outer membrane (sensu Gram-negative Bacteria); IEA.			
D	R	GO; GO:0005198;	F:structural molecule activity; IEA.			
D	R	InterPro; IPR006664;	Bac OmpA.			
D	R	InterPro; IPR001035;	MotY.			
D	R	InterPro; IPR002368;	OmpA.			
D	R	InterPro; IPR006665;	OmpA/MotB.			
D	R	InterPro; IPR006690;	OMPALIKE.			
D	R	InterPro; IPR000498;	OmpA_tmern.			
D	R	Pfam; PF00691;	OmpA_1.			
D	R	Pfam; PF01389;	OmpA membrane; 1.			
D	R	PRINTS; PR01023;	NAPLMOTY.			
D	R	PRINTS; PR01021;	OMPADOMAIN.			
D	R	PRINTS; PR01022;	OUTERMERANE.			
D	R	ProDom; PD000930;	OmpA/MotB_1.			
D	R	PROSITE; PS01068;	OMPAL_1.			
S	Q	SEQUENCE	346 AA; 37188 MW; 5736077E41BD84C3 CRC64;			
 Query Match						
Best Local Similarity 84.3%; Score 1505; DB 2; Length 346;						
Matches 284; Conservative 18; Mismatches 25; Indels 10; Gaps 2						
Q	y	6	VLNAAPKDNTWYAGKLGWSYHDTGFYGNQGQNNGPTRNDQLGAGAFGGYQVNPLYGF	65		
D	b	18	VAQAAPKDNWTWYTGAKLGWSYHDTGTF-----NNNGPTHEINQLGAGAFGGYQVNPLYGF	72		
Q	y	66	EMGYDWILGRWAYKGSVDNGAFKAOGVOLTAKLGYPIITDDLDIYTRLGGMWRADSKNYA	125		
D	b	73	EMGYDWILGRMPYKGSVENGAFAOGVOLTAKLGYPIITDDLDVYTRLGGMWRADTKSN--	130		
Q	y	126	STGYSRSEHDTGVSFPFAGGVVEAVTRDIATRLERYQWVNNIGDAHTIGTRPDNGMLSLGV	185		
D	b	131	---VGKKNHDTGVSVPFAGGVVEYAITPEIATRLERYQWVNNIGDAHTIGTRPDNGMLSLGV	187		
Q	y	186	SYRFGQEDAAAPVAPAPAPAEVATKHFTLKSDVLNFENKATLKPEGQAALDQLYTQLSN	245		
D	b	188	SYRFGQGEAAPVAPAPAPAEVQTKHFTLKSDVLNFENKATLKPEGQAALDQLYSOLSN	247		

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QY 246 MDPKGSVVLGYTDRIGSAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 248 LDPKGSVVLGYTDRIGSAYNQALSERRAQSVVDYLSKGPADKISARGMGESNPVT 307
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
Db 308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIDVVVTQP 344

RESULT 10
Q57QT3 SALCH PRELIMINARY; PRT; 350 AA.
AC Q57QT3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Putative hydrogenase, membrane component.
GN Name=ompA; OrderedLocusNames=SC1022;
OS Salmonella cholerae-suis (Salmonella enterica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
[1]
NCBI_TaxID=591;
RE NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RT Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
DR EMBL; AE017220; AAY64928.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 350 AA; 37491 MW; 7C3529A442E234FC CRC64;

Query Match 82.3%; Score 1501; DB 2; Length 350;
Best Local Similarity 83.1%; Pred. No. 7.1e-107;
Matches 280; Conservative 25; Mismatches 26; Indels 6; Gaps 2;

QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNQNGPTRNDOLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----NNDGPTHEHQLGAGAFGGYQVNPYVGF 72
QY 66 EMGYDNLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDDLDIYTRLGGMWRADSKGNYA 125
Db 73 EMGYDNLGRMPYKGDNINGAYKAGQVOLTAKLGYPTDDLDVYTRLGGMWRADTKSNVP 132
QY 126 STGVSRSRSHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
Db 133 G-GPSTKDHDTGVSVPFAGGIEVATPEIATRLLEYQWNTNIGDANTIGTRPDNGLLSVG 191
QY 186 SYRFGQEDAAPVVAAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 192 SYRFGQEEAAPVVAAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 251
QY 246 MDPKGSVVLGYTDRIGSAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 252 LDPKGSVVLGYTDRIGSDAYNQGLSEKRAQSVVDYLSKGPISNKGISARGMGESNPVT 311
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
Db 312 GNTCDNVKPRALIDCLAPDRRVEIEVKGIDVVVTQP 348

RESULT 11
Q5PGD5 SALPA
ID Q5PGD5 SALPA PRELIMINARY; PRT; 350 AA.
AC Q5PGD5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Outer membrane protein A.
```

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GN Name=ompA; OrderedLocusNames=SPAL1780;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 9150;
RX PubMed=15531882; DOI=10.1038/ngl470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Forwollik S., Sabo A., Meyer R., Bieri T., Ozerky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Naeh W., Miner T., Minx P.,
RA Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
DR EMBL; CP000026; AAV77696.1; -; Genomic_DNA.
DR SMR; Q5PGD5; 22-201.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR001035; MotY.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OMPA_LIKE.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01023; NAFEGMOTY.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMBRANE.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA; 1.
KW Complete proteome.
SQ SEQUENCE 350 AA; 37492 MW; 863F29A442EF8F91 CRC64;

Query Match 82.3%; Score 1500; DB 2; Length 350;
Best Local Similarity 83.1%; Pred. No. 8.5e-107;
Matches 280; Conservative 25; Mismatches 26; Indels 6; Gaps 2;

QY 6 VLNAAPKONTWYAGKLGWSQYHDTGFGYNGFNQNGPTRNDOLGAGAFGGYQVNPYLG 65
Db 18 VAQAAPKONTWYAGKLGWSQYHDTGFI-----NNDGPTHEHQLGAGAFGGYQVNPYVGF 72
QY 66 EMGYDNLGRMAYKGSVDNGAFKAGQVOLTAKLGYPTDDLDIYTRLGGMWRADSKGNYA 125
Db 73 EMGYDNLGRMPYKGDNINGAYKAGQVOLTAKLGYPTDDLDVYTRLGGMWRADTKSNVP 132
QY 126 STGVSRSRSHDTGVSVPFAGGVEMAVTRDIATRLLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
Db 133 G-GPSTKDHDTGVSVPFAGGIEVATPEIATRLLEYQWNTNIGDANTIGTRPDNGLLSVG 191
QY 186 SYRFGQEDAAPVVAAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 245
Db 192 SYRFGQEEAAPVVAAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 251
QY 246 MDPKGSVVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
Db 252 LDPKGSVVLGYTDRIGSDAYNQGLSEKRAQSVVDYLSKGPISNKGISARGMGESNPVT 311
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
Db 312 GNTCDNVKPRALIDCLAPDRRVEIEVKGIDVVVTQP 348

RESULT 12
OMPA_SALTI
ID OMPA_SALTI STANDARD; PRT; 350 AA.
AC Q827S0; Q7C962;
```

DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Outer membrane protein A precursor.
 GN Name=ompA; OrderedLocusNames=STV1091, t1850;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101614;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felkell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen R.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodyanni V., Schwartz B.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- FUNCTION: Required for the action of colicins K and L and for the
 CC stabilization of mating aggregates in conjugation. Serves as a
 CC receptor for a number of T-even like phages. Also acts as a porin
 CC with low permeability that allows slow penetration of small
 CC solutes (By similarity).
 CC -1- SUBUNIT: Monomer (Probable).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -1- SIMILARITY: Belongs to the ompA family.
 CC -1- SIMILARITY: Contains 1 OmpA-like domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AL627269; CAD08196.1; -; Genomic DNA.
 CC EMBL: AE016840; AA069468.1; -; Genomic DNA.
 CC HSSP: P02934; 1QJP.
 CC SHR: Q82750; 22-201.
 CC InterPro: IPR006664; Bac_OmpA.
 CC InterPro: IPR002368; OmpA.
 CC InterPro: IPR006665; OmpA/MotB.
 CC InterPro: IPR006690; OmpA LIKE.
 CC InterPro: IPR000498; OmpA_tmern.
 CC Pfam: PF00691; OmpA; 1.
 CC Pfam: PF01389; OmpA membrane; 1.
 CC PRINTS: PR01021; OMPADOMAIN.
 CC PRINTS: PR01022; OUTRMBRANEA.
 CC ProDom: PD000930; OmpA/MotB; 1.
 CC PROSITE: PS01088; OmpA_1; 1.
 CC PROSITE: PSS1123; OmpA_2; 1.
 CC Complete proteome; Conjugation; Ion transport; Membrane;
 CC Outer membrane; Phage recognition; Porin; Repeat; Signal;
 CC Transmembrane; Transport.
 KW SIGNAL 1 21 By similarity.
 KW CHAIN 22 350 Outer membrane protein A.
 FT TRANSMEM 27 40 Potential.
 FT TRANSMEM 55 67 Potential.

FT TRANSMEM 70 85 Potential.
 FT TRANSMEM 97 107 Potential.
 FT TRANSMEM 111 126 Potential.
 FT TRANSMEM 146 157 Potential.
 FT TRANSMEM 163 179 Potential.
 FT TRANSMEM 185 196 Potential.
 FT REPEAT 205 206 1.
 FT REPEAT 207 208 2.
 FT REPEAT 209 210 3.
 FT REPEAT 211 212 4.
 FT DOMAIN 214 342 OmpA-like.
 FT REGION 205 212 4 X 2 AA tandem repeats of A-P.
 FT DISULFID 315 327 By similarity.
 SQ SEQUENCE 350 AA; 37477 MW; EB90059DFCADF3 CRC64;
 Query Match 82.2%; Score 1499; DB 1; Length 350;
 Best Local Similarity 82.8%; Pred. No. 1e-106;
 Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;
 QY 6 VLNAAPKDNITWYAGGKLGMSQYHDTGFGYNGFNQNGPTRNDQLGAGAFGQYQVNPYLG 65
 DB 18 VAQAAPKDNITWYAGKLGMSQYHDTGFI----HNDGPTHENQLGAGAFGQYQVNPYVG 72
 QY 66 EMGYDWLGRMAYKGVNDGAFKAQGVQLTAKLGYPITDDLDIYTRLCGMVWRADSKGNYA 125
 DB 73 EMGYDWLGRMPYKGDNTNGAYKAQGVQLTAKLGYPITDDLDVYTRLCGMVWRADTKSNVP 132
 QY 126 STGVSRSEHDTGVSVPFAGSVGVAWTRDIATRLLEYQVNNIGDAGTVGTRPDNGMLSLV 185
 DB 133 G-GASTQKDHDTGVSVPFAGIEIATPEIATRLLEYQVNTNIGDANTIGTRPDNGLLSVG 191
 QY 186 SYRFGQEDAAPVAP 245
 DB 192 SYRFGQEDAAPVAP 251
 QY 246 MPKQGSVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGENPVT 305
 DB 252 LQPKDGSVVVLGFTDRIGSDAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGENPVT 311
 QY 306 GNTCDNVKARALIDCLAPDRRVEIEVKYKEVVTOP 342
 DB 312 GNTCDNVKARALIDCLAPDRRVEIEVKYKEVVTOP 348

RESULT 13

OMPA_SALTY STANDARD; PRT; 350 AA.
 AC P02936;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Outer membrane protein A precursor (Outer membrane protein 33K) (Outer
 DE membrane major heat-modifiable protein).
 GN Name=ompA; OrderedLocusNames=STM1070;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83287368; PubMed=6349993;
 RA Freidl R., Cole S.T.;
 RT "Cloning and molecular characterization of the ompA gene from
 RT Salmonella typhimurium.";
 RL Eur. J. Biochem. 134:497-502(1983).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL Ltr2";
CC Nature 413:852-856(2001).
CC -1- FUNCTION: Required for the action of collicins K and L and for the
CC stabilization of mating aggregates in conjugation. Serves as a
CC receptor for a number of T-even like phages. Also acts as a porin
CC with low permeability that allows slow penetration of small
CC solutes (By similarity).
CC -1- SUBUNIT: Monomer (Probable).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC -1- SIMILARITY: Belongs to the OmpA family.
CC -1- SIMILARITY: Contains 1 OmpA-like domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR ENBL; X02006; CAA26037.1; -; Genomic DNA.
DR ENBL; AE008746; AAL20003.1; -; Genomic DNA.
DR PIR; A03436; MMEBAT.
DR HSSP; P02934; 1QJP.
DR SMR; P02936; 22-201.
DR StyGene; SG10263; ompA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OmpA LIKE.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANE.
DR PRODOM; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA_1; 1.
DR PROSITE; PS1123; OMPA_2; 1.
KW Complete proteome; Conjugation; Ion transport; Membrane;
KW Outer membrane; Phage recognition; Porin; Repeat; Signal;
KW Transmembrane; Transport.
FT SIGNAL 1 21
FT CHAIN 22 350
FT TRANSMEM 27 40
FT TRANSMEM 55 67
FT TRANSMEM 70 85
FT TRANSMEM 97 107
FT TRANSMEM 111 126
FT TRANSMEM 146 157
FT TRANSMEM 163 179
FT TRANSMEM 185 196
FT REPEAT 205 206
FT REPEAT 207 208
FT REPEAT 209 210
FT REPEAT 211 212
FT DOMAIN 214 342
FT REGION 205 212
FT DISULFID 315 327
FT CONFLICT 114 114 V -> F (in Ref. 1).
FT CONFLICT 247 247 S -> I (in Ref. 1).
SQ SEQUENCE 350 AA; 37515 MW; B4AC52C8C5DF54FE CRC64;

Query Match 82.0%; Score 1495; DB 1; Length 350;
Best Local Similarity 82.0%; Pred. No. 2e-106;
Matches 279; Conservative 26; Mismatches 26; Indels 6; Gaps 2;

QY 6 VLNAAPKDNWTYAGKLGWSQYHDTGFGYNGFNNGNPNRNDOLGAGAFGGYQVNPYLG 65
DB 18 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----HNDGPTHEHQLGAGAFGGYQVNPYVGF 72

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADSKGNYA 125
DB 73 EMGYDWLGRMPYKGDNINGAYKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADTKSNVP 132

QY 126 STGVSRSEHDTGVSPVFAGGVEMAVTRDIATRLYQWVNNIGDAGTVGTRPDNGLSLGV 185
DB 133 G-GPSTKDHDTGVSPFAGGIEYAITPEIATRLYQWVNNIGDANTIGTRPDNGLSLGV 191
QY 186 SYRFGQEDAAPVAPAPAPAPAPAPVATKHFTLKSDVLFNFKATLKPEGQALDQLYTQLSN 245
DB 192 SYRFGQEDAAPVAPAPAPAPAPAPVATKHFTLKSDVLFNFKATLKPEGQALDQLYTQLSN 251
QY 246 MPKQGSADVILGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPACKISARGHGESNPVT 305
DB 252 LDPKQGSVVVLGFTDRIGSDAYNQQLSEKRAQSVVDYLISKGIPSKISARGHGESNPVT 311
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKYKEVWVTP 342
DB 312 GNTCDNVKARAALIDCLAPDRRVEIEVKYKDVVWVTP 348

RESULT 14
Q8CW76 ECOL6
ID Q8CW76_ECOL6 PRELIMINARY; PRT; 379 AA.
AC Q8CW76;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein A.
GN Name=ompA; OrderedLocustNames=c1093;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]_SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O6:HI / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AB016758; AAN79561.1; -; Genomic DNA.
DR HSSP; P02934; 1QJP.
DR SMR; Q8CW76; 51-230.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR001035; MotY.
DR InterPro; IPR002368; OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR InterPro; IPR006690; OMPA LIKE.
DR InterPro; IPR000498; OmpA_tmam.
DR Pfam; PF00691; OmpA; 1.
DR Pfam; PF01389; OmpA membrane; 1.
DR PRINTS; PR01023; NAFEGMOTY.
DR PRINTS; PR01021; OMPADOMAIN.
DR PRINTS; PR01022; OUTRMMBRANE.
DR PRODOM; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OmpA; 1.
KW Complete proteome.
SQ SEQUENCE 379 AA; 41054 MW; CE396D152EB1EDCA CRC64;

Query Match 81.6%; Score 1487; DB 2; Length 379;
Best Local Similarity 83.7%; Pred. No. 9.4e-106;
Matches 282; Conservative 17; Mismatches 32; Indels 6; Gaps 2;

QY 6 VLNAAPKDNWTYAGKLGWSQYHDTGFGYNGFNNGNPNRNDOLGAGAFGGYQVNPYLG 65
DB 47 VAQAAPKDNWTYAGKLGWSQYHDTGFI-----PNNGPTHEHQLGAGAFGGYQVNPYVGF 101

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMVWRADSKGNYA 125

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DR PRINTS; PRO1021; OMPADOMAIN.
DR PRINTS; PRO1022; OUTRMHBRANEA.
DR ProDom; PD000930; OmpA/MotB; 1.
DR PROSITE; PS01068; OMPA; 1.
KW Complete proteome.
SQ SEQUENCE 348 AA; 37283 MW; 42623C67041D62F4 CRC64;

Query Match      80.8%; Score 1473; DB 2; Length 348;
Best Local Similarity 83.4%; Pred. No. 9,9e-105;
Matches 281; Conservative 18; Mismatches 30; Indels 8; Gaps 3;

QY      6  VLNAAPKDN TWYAGGKLGHSQYHDTGTFYGN GPFQNNNGPTRNDOLGAGAFGGYQVNPYLG 65
DB      18  VAQAAPKDN TWYTGAKLGHSQYHDTGFI-----PNNGP THENOLGAGAFGGYQVNPYVG 72

QY      66  EMGYDNLGRMAYKGSVDNGAFKAQGVQLTAKLGYPIITDDLDIYTRLCGMVWRADSKGNYA 125
DB      73  EMGYDNLGRMPYKGDNINGAYKAQGVQLTAKLGYPIITDDLDIYTRLCGMVWRADTKANVP 132

QY      126 STGVSREHDTGVSVPFAGGVAVTRDIATRLLEYQWVNNIGDAGTVGTTRPDNGMLSLGV 185
DB      133 G-GASFKDHD TGVSVPFAGGVEYAITPEIATRLLEYQWVNNIGDANTIGTRPDNGLLSLGV 191

QY      186 SYRFGQEDAAPVVA PAPAPAEVATKFTLKSDVLFNFNFKATLKPEGQQAALDOLYTOLSN 245
DB      192 SYRFGQGEAAPV--APAPAEVQTKFTLKSDVLFNFNFKATLKPEGQQAALDOLYTOLSN 249

QY      246 MDPKDGSAVVLGYTDRIGSEAYNQOLSEKPAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
DB      250 LDPKDGSVVLGYTDRIGSDAYNQGLSERRAQSVVDYLVISKGIPADKISARGMGESNPVT 309

QY      306 GNTCDNVKQAAALIDCLAPDRRVEIEVKGYKEVVTQP 342
DB      310 GNTCDNVKQAAALIDCLAPDRRVEIEVKGIKDVVTQP 346

Search completed: November 26, 2005, 00:09:44
Job time : 232 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2005, 23:59:49 ; Search time 40 Seconds
(without alignments)
827.464 Million cell updates/sec

Title: US-09-913-772A-2

Perfect score: 1823

Sequence: 1 MKAIFVLNAAPKONTWYAGS.....DRRVEIEVKGYKEVVTQPA 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1782	97.8	356	2 JC6558	outer membrane pro
2	1542	84.6	350	2 J07222	outer membrane pro
3	1525.5	83.7	351	1 MMEBAD	outer membrane pro
4	1511	82.9	346	1 MMECA	outer membrane pro
5	1511	82.9	346	2 A90759	outer membrane pro
6	1511	82.9	346	2 G85622	outer membrane pro
7	1499	82.2	350	2 A10626	outer membrane pro
8	1490	81.7	350	1 MMEBAT	outer membrane pro
9	1381.5	75.8	359	2 S07298	outer membrane pro
10	1325.5	72.7	353	2 AD0175	probable outer mem
11	1128.5	61.9	238	2 I62385	outer membrane pro
12	1112.5	61.0	244	2 I62393	outer membrane pro
13	1111	60.9	243	2 I62388	outer membrane pro
14	1110.5	60.9	244	2 I62389	outer membrane pro
15	1109	60.8	243	2 I84531	outer membrane pro
16	1106	60.7	243	2 I62386	outer membrane pro
17	1089	59.7	241	2 I62387	outer membrane pro
18	1084	59.5	241	2 I62391	outer membrane pro
19	1074.5	58.9	240	2 I62394	outer membrane pro
20	1056.5	58.0	238	2 I40703	outer membrane pro
21	646.5	35.5	353	2 C64187	outer membrane pro
22	515	28.3	349	2 B84968	outer membrane pro
23	443.5	24.3	321	2 F82104	outer membrane pro
24	271	14.9	194	2 A45275	21K outer membrane
25	262	14.4	236	2 A27894	outer membrane pro
26	255	14.0	242	2 C81205	outer membrane pro
27	251	13.8	240	2 A37004	outer membrane cla
28	250	13.7	242	2 A81782	outer membrane pro
29	243	13.3	326	2 S20494	root adhesin - Pse

30	231.5	12.7	350	2 S39156	outer membrane pro
31	227.5	12.5	407	2 H87341	OmpA family protei
32	208.5	11.4	319	2 C81294	outer membrane fib
33	206	11.3	344	2 A39139	outer membrane pro
34	206	11.3	389	2 B82819	outer membrane pro
35	199	10.9	210	2 A83516	probable outer mem
36	193.5	10.6	449	2 D87682	OmpA family protei
37	179	9.8	219	2 S47773	hypothetical 22.2K
38	176.5	9.7	261	2 E83185	probable outer mem
39	176	9.7	220	2 AC0982	probable outer mem
40	174	9.5	219	2 E91183	probable outer mem
41	174	9.5	219	2 A86030	probable outer mem
42	173.5	9.5	326	2 H70782	probable ompA prot
43	171.5	9.4	420	2 H95302	probable membrane
44	170	9.3	223	2 C82230	probable lipoprote
45	169.5	9.3	237	2 A83541	hypothetical prote

ALIGNMENTS

RESULT 1

JC6558

outer membrane protein A precursor - Klebsiella pneumoniae

C;Species: Klebsiella pneumoniae

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999

C;Accession: JC6558

R;Nguyen, T.N.; Samuelson, P.; Sterky, F.; Merle-Poitte, C.; Robert, A.; Baussant, T.; H

Gene 210, 93-101, 1998

A;Title: Chromosomal sequencing using a PCR-based biotin-capture method allowed isolation

A;Reference number: JC6558; MUID:98192544; PMID:9524233

A;Accession: JC6558

A;Molecule type: DNA

A;Residues: 1-356 <NGU>

A;Cross-references: UNIPARC:UPI00001780DF

A;Experimental source: IP I145

C;Genetics:

A;Gene: ompA

C;Superfamily: outer membrane protein A

C;Keywords: membrane protein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-356/Product: outer membrane protein A #status predicted <MAT>

Query Match 97.8%; Score 1782; DB 2; Length 356;

Best Local Similarity 99.4%; Pred. No 1.1e-127;

Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 VLNAAPKDNWTYAGGKLGWSQYHDTGYGNGFONNNGPTRNDQLGAGAFGGYQVNPYLGF 65

Db 18 VAQAAPKDNWTYAGGKLGWSQYHDTGYGNGFONNNGPTRNDQLGAGAFGGYQVNPYLGF 77

QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDDLDIYTRLGGWWRADSKGNYA 125

Db 78 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDDLDIYTRLGGWWRADSKGNYA 137

QY 126 STGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLVEYQVNNIGDAGTVGTRPDNGMLSLGV 185

Db 138 STGVSRSEHDTGVSVPFAGGVEWAVTRDIATRLVEYQVNNIGDAGTVGTRPDNGMLSLGV 197

QY 186 SYRFGQEDAAPVVPAPAPAPAPAVATKHFTLKSDVLFNFKATLKPQEQQALDQLYTOLSN 245

Db 198 SYRFGQEDAAPVVPAPAPAPAVATKHFTLKSDVLFNFKATLKPQEQQALDQLYTOLSN 257

QY 246 MDPKGSADVLTGTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGHGESNPVT 305

Db 258 MDPKGSADVLTGTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGHGESNPVT 317

QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA 343

Db 318 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA 355

RESULT 2

A;Experimental source: strain O157:H7, substrain RMD 05099S2
C;Genetics:
A;Gene: ECol1041
C;Superfamily: outer membrane protein A

Query Match 82.9%; Score 1511; DB 2; Length 346;
Best Local Similarity 84.9%; Pred. No. 3.9e-107;
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTWYAGGKLGSQYHDTGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLGF 65
DB 18 VAQAAPKDNWTWYTGAKLGSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVG 72
QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVLTAKLGPITDDLDIYTRLGGMVMWRADSKGNYA 125
DB 73 EMGYDWLGRMPYKGSVENGAQYKAQGVLTAKLGPITDDLDIYTRLGGMVMWRADTKSN-- 130
QY 126 STCVSRSEHDTGVSVPFAGGVAVMTDRIATRLLEYQWVNIGDAGTVGTPDNGMLSLGV 185
DB 131 ---VYGKNHDTGVSVPFAGGVAVITPEIATRLEYQWVNIGDAHTIGTTPDNGMLSLGV 187
QY 186 SYRFGGEDAAPVVAAPAPAPEVATKHFTLKSDVLFNFNKATULKPEGQALDOLYTOLS 245
DB 188 SYRFGGEAAPVVAAPAPAPEVQTGHFTLKSDVLFNFNKATULKPEGQALDOLYTOLS 247
QY 246 MDPKGSAVVLYGTYDRIGSAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
DB 248 LDPKGSSVVLYGTYDRIGSDAYNQLSERRAQSVVDYLSIKGIPADKISARGMGESNPVT 307
QY 306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYEVVTP 342
DB 308 GNTCDNVKORAALIDCLAPDRRVEIEVKGIKDVTTP 344

RESULT 6
G85622
outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain RMD 05099S2)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85622
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Diallanca, E.; Potamousis, K.; Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <TO>
A;Cross-references: UNIPROT:P02934; UNIPARC:UPI0000130CF0; GB:AE005174; NID:g12
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A

Query Match 82.9%; Score 1511; DB 2; Length 346;
Best Local Similarity 84.9%; Pred. No. 3.9e-107;
Matches 286; Conservative 17; Mismatches 24; Indels 10; Gaps 2;

QY 6 VLNAAPKDNWTWYAGGKLGSQYHDTGYNGFONNNGPTRNDOLGAGAFGGYQVNPYLGF 65
DB 18 VAQAAPKDNWTWYTGAKLGSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVG 72
QY 66 EMGYDWLGRMAYKGSVDNGAFKAQGVLTAKLGPITDDLDIYTRLGGMVMWRADSKGNYA 125
DB 73 EMGYDWLGRMPYKGSVENGAQYKAQGVLTAKLGPITDDLDIYTRLGGMVMWRADTKSN-- 130
QY 126 STCVSRSEHDTGVSVPFAGGVAVMTDRIATRLLEYQWVNIGDAGTVGTPDNGMLSLGV 185
DB 131 ---VYGKNHDTGVSVPFAGGVAVITPEIATRLEYQWVNIGDAHTIGTTPDNGMLSLGV 187
QY 186 SYRFGGEDAAPVVAAPAPAPEVATKHFTLKSDVLFNFNKATULKPEGQALDOLYTOLS 245

Best Local Similarity 78.2%; Pred. No. 2.7e-97;
Matches 269; Conservative 24; Mismatches 44; Indels 7; Gaps 4;

QY 6 VLNAAPKNDNTWYAGGKLGWSQYHDTGFGNGFQ--NNGPTRNDOLGAGAGGQYQVNPYL 63
DB 18 VAQAAPKNDNTWYTGAKLGNQYHDTGFGNGYNGINGPHTKDKQLGAGAGFLGQANQYL 77

QY 64 GPEMGYDLMGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKGN 123
DB 78 GFELGYDLMGRMPYKGSVNNAGAFKAQGVQLAALKLSYPIADLDIYTRLGGMWRADSKAN 137

QY 124 YASTGVSRSSEHDTGVSVPFAGGVWAVTRDIATRLFYQWNNIGDAGTGTGTRPDNGMLSL 183
DB 138 YGRTGQRLSDHDTGVSPLAAGVVEYALTKWATRLDYQFVNSIGDAGTGTGTRPDNTWLSL 197

QY 184 GVSRYRFGQED--AAPVVAAPAPAPAEVATKFTLKSVDVLFNFKATLKPEGQALDQLYTQ 242
DB 198 GVSRYRFGQDDVAP--APAPAPAPVETKFTLKSVDVLFNFKATLKPEGQALDQLYTQ 255

QY 243 LSNMPPKGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
DB 256 LSNMPPKGSVAVLGYTDAVGSQYQNLSEKRAQSVVDYLVAKGIPSDKISARGMGESN 315

QY 303 PVTGNTCDNVKARA--ALIDCLAPDRRVEIEVKYKEVVTQAP 344
DB 316 AVTGNTCGYKSGRATKAQIVCLAPDRRVEIEVKYKEVVTQAPQ 359

RESULT 10
AD0175
probable outer membrane porin A protein ompA [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD0175
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-farraga, A.M.; Chillingworth, T.; Cronan, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <RES>
A;Cross-references: UNIPROT:Q8ZG77; UNIPARC:UPI00000CD7EA; GB:AL590842; PIDN:CAC90263.1;
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A

Query Match 72.7%; Score 1325.5; DB 2; Length 353;
Best Local Similarity 75.2%; Pred. No. 4.8e-93;
Matches 255; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

QY 6 VLNAAPKNDNTWYAGGKLGWSQYHDTGFGNGFQNNNGPTRNDOLGAGAGGQYQVNPYLGF 65
DB 18 VAQAAPKNDNTWYTGAKLGNQYHDTGFGNGYNGINGPHTKDKQLGAGAGFLGQANQYLGF 73

QY 66 EMGYDLMGRMAYKGSVDNGAFKAQGVQLTAKLGYPTDLDIYTRLGGMWRADSKGNYA 125
DB 74 EMGYDLMGRMPYKGSVNNAGAFKAQGVQLAALKLSYPIADLDIYTRLGGMWRADSKGSP- 132

QY 126 STGVSRSSEHDTGVSVPFAGGVWAVTRDIATRLFYQWNNIGDAGTGTGTRPDNGMLSL 184
DB 133 DGGLDRASGHDTGVSPLVALGABYAWTKWATRMVQWNNIGDAGTGTGTRPDNGMLSL 192

QY 185 VSYRFGQED--AAPVVAAPAPAPAEVATKFTLKSVDVLFNFKATLKPEGQALDQLYTQ 243
DB 193 VSYRFGQEDAAAPVVAAPAPAPAEVATKFTLKSVDVLFNFKATLKPEGQALDQLYTQ 252

QY 244 SNMPPKGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPAGKISARGMGESNP 303
DB 253 SSIDPPKGSVAVLGYTDRIGSEAYNQOLSEKRAQSVVDYLVAKGIPADKITARGEQANP 312

QY 304 VTGNTCDNVKARAALIDCLAPDRRVEIEVKYKEVVTQAP 342
DB 313 VTGNTCDNVKAPRAALIECLAPDRRVEIEVKYKEVVTQAP 351

RESULT 11
I62385
outer membrane protein ompA - Escherichia vulneris (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia vulneris
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62385
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62385
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-238 <RES>
A;Cross-references: UNIPROT:Q99114; UNIPARC:UPI00000B0580; GB:M63348; NID:q146984; PIDN:
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;98-109/Region: alanine/proline-rich

Query Match 61.9%; Score 1128.5; DB 2; Length 238;
Best Local Similarity 90.1%; Pred. No. 2.5e-78;
Matches 219; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

QY 93 LTAKLGPITDLDIYTRLGGMWRADSKGNVASTGVSRSSEHDTGVSVPFAGGVWAVTR 152
DB 1 LTAKLGPITDLDIYTRLGGMWRADSKGNVASTGVSRSSEHDTGVSVPFAGGVWAVTR 55

QY 153 DIATRLFYQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAAPVVAAPAPAEVATKH 212
DB 56 DIATRLFYQWNNIGDAGTGTGTRPDNGMLSLGVSYRFGQEDAAAPVVAAPAPAEVATKH 115

QY 213 FTLSKSDVLFNFKATLKPEGQALDQLYTQLSNMPPKGSVAVLGYTDRIGSEAYNQOLS 272
DB 116 FTLSKSDVLFNFKATLKPEGQALDQLYTQLSNMPPKGSVAVLGYTDRIGSEAYNQOLS 175

QY 273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
DB 176 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 235

QY 333 KGY 335
DB 236 KGY 238

RESULT 12
I62393
outer membrane protein ompA - Escherichia vulneris (ATCC 33822) (fragment)
N;Alternate names: outer membrane protein II
C;Species: Escherichia vulneris
A;Variety: ATCC 33822
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62393
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: I40701; MUID:92065252; PMID:1955870
A;Accession: I62393
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-244 <RES>
A;Cross-references: UNIPROT:Q47880; UNIPARC:UPI00000B0580; GB:M63350; NID:q147000; PIDN:
A;Experimental source: ATCC 33822
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A

C;Keywords: membrane protein	
F;104-115/Region: alanine/proline-rich	
Query Match	61.0%; Score 1112.5; DB 2; Length 244;
Best Local Similarity	87.2%; Pred. No. 4.2e-77;
Matches	212; Conservative 15; Mismatches 15; Indels 1; Gaps 1;
QY	93 LTAALGVPITDDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGSPVPAGGVEWAVTR 152
Db	1 LTAALGVPITDDLDIYTRLGGMWRADSKAQVPGTGASFKDHDGTGSPVPAGGVEWAMTR 60
QY	153 DIATRLVQWNNIGDAGTVGTRPDNGMLSLGVSYSRFG-QEDAAPVAVAPAPAPAVATK 211
Db	61 DIATRLVQWNNIGDAGTVGTRPDNGMLSLGVSYSRFGQEDVAVPVAVAPAPAPAVQVSTK 120
QY	212 HFTLKSDFLNFNFKATLKPEGQALDQLYTQLSNMDPKDGSVAVLGYTDRIQSEAYNQQL 271
Db	121 HFTLKSDFLNFNFKATLKPEGQALDQMYSQLSLNDPKDGSVVVLGFTDRIGSDAYNQGL 180
QY	272 SEKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
Db	181 SEKRAQSVVDYLSKGIPIKSNKISARGMGESNPVTGNTCDNVKARPALIDCLAPDRRVEIE 240
332 VKG 334	
241 VKG 243	
RESULT 13	
I62388	
outer membrane protein A - Escherichia fergusonii (ATCC 35472) (fragment)	
N;Alternate names: outer membrane protein II	
C;Species: Escherichia fergusonii	
A;Variety: ATCC 35472	
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004	
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.	
A;Title: Molecular and evolutionary relationships among enteric bacteria.	
A;Reference number: 140701; PMID:92065252; PMID:1955870	
A;Accession: I62388	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA	
A;Residues: 1-243 <RES>	
A;Cross-references: UNIPROT:P24747; UNIPARC:UPI0000130CF3; GB:M63352; NID:g146990; PIDN:	
A;Experimental source: ATCC 35471	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA	
A;Residues: 1-243 <RE2>	
A;Cross-references: UNIPARC:UPI0000130CF3; GB:M63353; NID:g146998; PIDN:AAA24240.1; PID:	
A;Experimental source: ATCC 35472	
C;Genetics:	
A;Gene: ompA	
C;Superfamily: outer membrane protein A	
C;Keywords: membrane protein	
F;103-114/Region: alanine/proline-rich	
Query Match	60.9%; Score 1111; DB 2; Length 243;
Best Local Similarity	87.2%; Pred. No. 5.5e-77;
Matches	211; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
QY	93 LTAALGVPITDDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGSPVPAGGVEWAVTR 152
Db	1 LTAALGVPITDDLDIYTRLGGMWRADTKAHNNVTGESEKNHDTGSPVPAGGVEWATP 60
QY	153 DIATRLVQWNNIGDAGTVGTRPDNGMLSLGVSYSRFGQEDAAPVAVAPAPAPAVATKH 212
Db	61 DIATRLVQWNNIGDAGTVGTRPDNGMLSLGVSYSRFGQEDAAPVAVAPAPAPAVQVTKH 120
QY	213 FTLKSDVLFNFKATLKPEGQALDQLYTQLSNMDPKDGSVAVLGYTDRIQSEAYNQQLS 272
Db	121 FTLKSDVLFNFKATLKPEGQALDQLYSQLSLNDPKDGSVVVLGFTDRIGSDAYNQGLS 180
C;Keywords: membrane protein	
F;104-115/Region: alanine/proline-rich	
Query Match	61.0%; Score 1112.5; DB 2; Length 244;
Best Local Similarity	87.2%; Pred. No. 4.2e-77;
Matches	212; Conservative 15; Mismatches 15; Indels 1; Gaps 1;
QY	93 LTAALGVPITDDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGSPVPAGGVEWAVTR 152
Db	1 LTAALGVPITDDLDIYTRLGGMWRADSKAQVPGTGASFKDHDGTGSPVPAGGVEWAMTR 60
QY	153 DIATRLVQWNNIGDAGTVGTRPDNGMLSLGVSYSRFG-QEDAAPVAVAPAPAPAVATK 211
Db	61 DIATRLVQWNNIGDAGTVGTRPDNGMLSLGVSYSRFGQEDVAVPVAVAPAPAPAVQVSTK 120
QY	212 HFTLKSDFLNFNFKATLKPEGQALDQLYTQLSNMDPKDGSVAVLGYTDRIQSEAYNQQL 271
Db	121 HFTLKSDFLNFNFKATLKPEGQALDQMYSQLSLNDPKDGSVVVLGFTDRIGSDAYNQGL 180
QY	272 SEKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
Db	181 SEKRAQSVVDYLSKGIPIKSNKISARGMGESNPVTGNTCDNVKARPALIDCLAPDRRVEIE 240
332 VKG 334	
241 VKG 243	
RESULT 14	
I62389	
outer membrane protein ompA - Escherichia vulneris (ATCC 33821) (fragment)	
N;Alternate names: outer membrane protein II	
C;Species: Escherichia vulneris	
A;Variety: ATCC 33821	
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004	
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.	
A;Title: Molecular and evolutionary relationships among enteric bacteria.	
A;Reference number: 140701; PMID:92065252; PMID:1955870	
A;Accession: I62389	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: DNA	
A;Residues: 1-244 <RES>	
A;Cross-references: UNIPROT:Q99115; UNIPARC:UPI000008BFF1D; GB:M63349; NID:g146992; PIDN:	
A;Experimental source: ATCC 33821	
C;Genetics:	
A;Gene: ompA	
C;Superfamily: outer membrane protein A	
C;Keywords: membrane protein	
F;104-115/Region: alanine/proline-rich	
Query Match	60.9%; Score 1110.5; DB 2; Length 244;
Best Local Similarity	86.8%; Pred. No. 6e-77;
Matches	211; Conservative 16; Mismatches 15; Indels 1; Gaps 1;
QY	93 LTAALGVPITDDLDIYTRLGGMWRADSKGNVASTGVSRSEHDTGSPVPAGGVEWAVTR 152
Db	1 LTAALGVPITDDLDIYTRLGGMWRADAKSQVGGTGASFKDHDGTGSPVPAGGVEWAMTR 60
QY	153 DIATRLVQWNNIGDAGTVGTRPDNGMLSLGVSYSRFG-QEDAAPVAVAPAPAPAVATK 211
Db	61 DIATRLVQWNNIGDAGTVGTRPDNGMLSLGVSYSRFGQEDVAVPVAVAPAPAPAVQVSTK 120
QY	212 HFTLKSDFLNFNFKATLKPEGQALDQLYTQLSNMDPKDGSVAVLGYTDRIQSEAYNQQL 271
Db	121 HFTLKSDFLNFNFKATLKPEGQALDQMYSQLSLNDPKDGSVVVLGFTDRIGSDAYNQGL 180
QY	272 SEKRAQSVVDYLVAKGIPACKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
Db	181 SEKRAQSVVDYLSKGIPIKSNKISARGMGESNPVTGNTCDNVKARPALIDCLAPDRRVEIE 240
332 VKG 334	
241 VKG 243	
RESULT 15	
I84531	
outer membrane protein A - Escherichia fergusonii (ATCC 35469) (fragment)	
N;Alternate names: outer membrane protein II	
C;Species: Escherichia fergusonii	
A;Variety: ATCC 35469	
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004	
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.	
A;Title: Molecular and evolutionary relationships among enteric bacteria.	
A;Reference number: 140701; PMID:92065252; PMID:1955870	
A;Accession: I84531	
A;Status: preliminary; translated from GB/EMBL/DBJ	

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